

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
1015	2adr	957	1015	6.8e-18	-0.01	0.80			ADRI; CHAIN: NULL;	ADR1, ZINC FINGER, NMR TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1015	2drp	A	372	428	3.4e-06	-0.30	0.11		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
1015	2drp	A	501	556	8.5e-10	-0.47	0.01		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
1015	2gli	A	354	428	3.4e-18	-0.36	0.21		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gli	A	358	467	1.5e-26	-0.44	0.10		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gli	A	404	556	6.8e-33	-0.34	0.71		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gli	A	451	583	8.5e-33	-0.29	0.28		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gli	A	479	593	5.1e-28	-0.67	0.15		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;

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									GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gli	A	901	1010	1e-33	-0.18	0.96	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	7znf			985	1013	3.4e-05	-0.23	0.31	ZINC FINGER DNA BINDING DOMAIN ZINC-FINGER (ZFY-SWAP) (NMR, 12 STRUCTURES) 7ZNF 3
1021	2ooc	A	1	299	3.4e-88	0.01	-0.17	CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q,	OXIDOREDUCTASE; FERROCYTOCHROME C:OXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE
1023	1amu	A	48	610	0			139.53	GRAMICIDIN SYNTHETASE I; CHAIN: A, B; PHENYLALANINE; CHAIN: C, D;
1023	1lci			59	608	0		133.28	LUCIFERASE; CHAIN: NULL; OXIDOREDUCTASE, MONOOXYGENASE, PHOTOPROTEIN, LUMINESCENCE
1028	1alh	A	98	184	3.4e-29			76.54	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;
1028	1mey	C	157	239	1.7e-50			97.35	DNA; CHAIN: A, B, D, E; COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;

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1028	1if6	A	97	269	1.4e-36		106.38		TEIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1028	1iib	C	130	239	6.8e-35		87.68		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1028	2gli	A	99	240	3.4e-31		87.54		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1029	1bih	A	1	351	6.8e-48		65.92		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, IFS-BINDING, HOMOPHILIC ADHESION
1029	1eap	B	133	348	1.7e-10		55.72		CATALYTIC ANTIBODY 1TE8 COMPLEXED WITH PHENYL [1-(1-N-SUCCINYLAMINOPOENTYL] 1EAP 3 PHOSPHONATE 1EAP 4	
1029	1iitb	B	54	353	1.7e-34		51.71		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE,

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										GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR) COMPLEX
1029	1kb5	H	133	351	1.7e-08			59.81	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	TCR VAPLHA VBETA DOMAIN-T-CELL RECEPTOR, 2 AND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
1029	1ma m	H	139	349	1.2e-11			56.22	IMMUNOGLOBULIN ANTIGEN-BINDING FRAGMENT (FAB) (IGG2B, KAPPA) IMAM 3	
1031	luby		57	398	5.1e-66	-0.31	0.11		FARNESYL DIPHOSPHATE SYNTHASE; CHAIN: NULL;	TRANSFERASE FPS; TRANSFERASE, ISOPRENE BIOSYNTHESIS, CHOLESTEROL BIOSYNTHESIS
1031	luby		65	397	5.1e-66			70.74	FARNESYL DIPHOSPHATE SYNTHASE; CHAIN: NULL;	TRANSFERASE FPS; TRANSFERASE, ISOPRENE BIOSYNTHESIS, CHOLESTEROL BIOSYNTHESIS
1032	1dfn	A	132	161	1.1e-12			58.55	DEFENSIN DEFENSIN /HNP\$-3	
1032	1dfn	A	133	161	1.1e-12	-0.35	1.00		DEFENSIN DEFENSIN /HNP\$-3	
1032	1dfn	A	133	161	5.1e-11	-0.35	1.00		DEFENSIN DEFENSIN /HNP\$-3	
1034	1a4y	A	66	224	5.7e-22	-0.15	0.35		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE); COMPLEX (R1-ANG).HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1034	1a9n	A	68	208	3.8e-24	0.44	0.78		U2 RNA HAIRPIN IV; CHAIN: Q,	COMPLEX (NUCLEAR)

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									R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	PROTEIN(RNA) COMPLEX (NUCLEAR PROTEIN(RNA)), RNA, SNRNP, RIBONUCLEOPROTEIN
1034	1a9n	A	93	249	1.3e-21	0.15	0.57		U2 RNA HARPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN(RNA)) COMPLEX (NUCLEAR PROTEIN(RNA)), RNA, SNRNP, RIBONUCLEOPROTEIN
1034	1a9n	C	68	208	1.1e-23	0.52	0.80		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN(RNA)) COMPLEX (NUCLEAR PROTEIN(RNA)), RNA, SNRNP, RIBONUCLEOPROTEIN
1034	1a9n	C	93	249	9.5e-21	0.21	0.62		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN(RNA)) COMPLEX (NUCLEAR PROTEIN(RNA)), RNA, SNRNP, RIBONUCLEOPROTEIN
1034	1cs6	A	279	363	3.8e-06	0.12	0.05		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1034	1cvs	C	283	364	7.6e-07	0.27	0.22		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1034	1cvs	D	283	367	1.5e-06	0.15	0.25		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1034	1d0b	A	39	186	8.5e-19	0.22	0.74		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1034	1d0b	A	44	223	1.9e-24	0.13	0.58		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL

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1034	1dce	A	106	218	1e-09	-0.25	0.03		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B; D;	ADHESION TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N. FORMYL METHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1034	1dce	A	38	235	1.9e-16	0.05	-0.01		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B; D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N. FORMYL METHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1034	1ds9	A	104	245	1e-08	-0.76	0.10		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS FLAGELLA
1034	1ds9	A	45	208	7.6e-21	-0.56	0.04		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS FLAGELLA
1034	1epf	A	279	358	5.7e-07	0.10	0.98		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1034	1ev2	E	276	373	1.5e-06	0.15	0.33		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (Ig)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1034	1ev2	G	283	358	3.8e-06	0.12	0.77		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2;

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								FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	IMMUNOGLOBULIN (Ig) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN Ig-LIKE DOMAINS. BTREFOIL FOLD.
1034	1foj	A	183	230	0.00013	-0.40	0.25	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP_RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1034	1foj	B	183	236	0.00076	-0.61	0.05	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP_RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1034	1tit		280	356	5.7e-06	0.21	0.01	TITIN; CHAIN: NULL;	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN (27, TITIN Ig REPEAT 27, MUSCLE PROTEIN, IMMUNOGLOBULIN-LIKE DOMAIN
1034	1tnm		279	358	1.7e-06	0.23	0.34	MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58
1034	1www	X	394	490	1.7e-09	0.25	-0.19	NERVE GROWTH FACTOR; CHAIN: V, W; TRKA RECEPTOR; CHAIN: X, Y;	NERVE GROWTH FACTOR/TRKA COMPLEX BETA-NGF; COMPLEX, TRKA RECEPTOR, NERVE GROWTH FACTOR, CYSTEINE KNOT, 2 IMMUNOGLOBULIN LIKE DOMAIN, NERVE GROWTH FACTOR/TRKA COMPLEX
1034	1yrg	A	44	198	7.6e-19	-0.34	0.24	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING,

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1034	3nem	A	279	358	9.5e-07	0.40	0.46		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	HEMIEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1035	1cke	A	360	519	0.0019	-0.10	0.12		CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE CK, MSSA; NUCLEOTIDE MONOPHOSPHATE KINASE,, TRANSFERASE
1035	1coz	A	193	312	1.1e-11	0.18	0.18		GLYCEROL-3-PHOSPHATE CYTIDYL TRANSFERASE; CHAIN: A,B;	TRANSFERASE,APS TRANSFERASE,APS KINASE, ADENYLYLSULFATE KINASE, SULFATE, NUCLEOTIDE 2 KINASE, TRANSFERASE
1035	1d6j	A	359	393	1.9e-05	-0.55	0.35		ADENOSINE-SPHOSPHOSULFATE KINASE; CHAIN: A, B;	TRANSFERASE,APS KINASE, ADENYLYLSULFATE KINASE, SULFATE, NUCLEOTIDE 2 KINASE, TRANSFERASE
1038	1eth	A	1	319	0			112.24	TRIACYLGLYCEROL ACYL-HYDROLASE; CHAIN: A, C; COLIPASE; CHAIN: B, D	COMPLEX (HYDROLASE/COFACTOR), LIPID DEGRADATION
1038	1ep1		2	316	0			107.65	RP2 LIPASE; CHAIN: NULL;	SERINE ESTERASE RELATED PROTEIN 2 LIPASE; SERINE ESTERASE, HYDROLASE, LIPID DEGRADATION, PANCREAS, 2 GLYCOPROTEIN, CHIMERIC

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1038	1hp1	A	I	318	0		107.77	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) (TRIACYL GLYCEROL HYDROLASE) (PPL_3)	
1038	1lpb	B	I	316	0		109.40	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED ILPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) ILPB 4	
1038	1lp1	2		316	0		100.01	PANCREATIC LIPASE RELATED PROTEIN 1; CHAIN: NULL;	HYDROLASE HYDROLASE, LIPID DEGRADATION, PANCREATIC LIPASE
1044	1ahd	P	154	219	3.4e-34	0.19	1.00	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1044	1au7	A	145	213	3.8e-26	-0.39	0.65	PIT-1; CHAIN: A; B; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) GHF-1; COMPLEX (DNA-BINDING PROTEIN/DNA), PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR
1044	1b72	A	158	215	1.7e-27	0.20	1.00	HOMEBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1044	1b8i	A	158	212	5.1e-29	0.33	1.00	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEBOX PROTEIN	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN,

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									EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	HOMEOTIC PROTEINS, DEVELOPMENT 3 SPECIFICITY
1044	1fj1	A	*	153	213	7.6e-26	0.16	1.00	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN; DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1044	1fj1	B		155	211	1.9e-23	0.09	1.00	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN; DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1044	1ftt			155	216	1.9e-23	0.03	0.96	THYROID TRANSCRIPTION FACTOR 1 HOMEODOMAIN; IFTT 6 CHAIN: NULL; IFTT 7	DNA BINDING PROTEIN TTF-1 HD; IFTT 8 DNA BINDING PROTEIN, HOMEODOMAIN, TRANSCRIPTION FACTOR IFTT 19
1044	1fz2			153	212	5.1e-29	0.16	0.99	DNA-BINDING FUSHI TARazu PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ_3	
1044	1nk2	P		146	223	6.8e-20			HOMEBOX PROTEIN VND; CHAIN: P; DNA; CHAIN: A, B;	COMPLEX (HOMEODOMAIN/DNA) VND/NK-2 HOMEODOMAIN, VENTRAL NERVOUS SYSTEM HOMEODOMAIN, HOMEobox, DNA-BINDING PROTEIN, EMBRYONIC 2 DEVELOPMENT, COMPLEX (HOMEODOMAIN/DNA)
1044	1nk3	P		153	215	1.9e-25	0.26	1.00	HOMEBOX PROTEIN VND; CHAIN: P; DNA; CHAIN: A, B;	COMPLEX (HOMEODOMAIN/DNA) VND/NK-2 HOMEODOMAIN, VENTRAL NERVOUS SYSTEM HOMEODOMAIN, HOMEobox, DNA-BINDING PROTEIN, EMBRYONIC 2 DEVELOPMENT, COMPLEX (HOMEODOMAIN/DNA) HELIX
1044	1san			160	219	8.5e-32	0.30	0.99		DNA-BINDING PROTEIN

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									ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	
1046	1a4y	A	41	214	0.0095	0.27	0.46		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE); COMPLEX (INHIBITOR/NUCLEASE); COMPLEX (R-LANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1048	1cfc	A	6	187	6.8e-22	-0.08	0.40		CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A; ₅	TRANSFERASE CK, MSSA; NUCLEOTIDE MONOPHOSPHATE KINASE,, TRANSFERASE
1048	1d6j	A	3	187	3.4e-23	0.08	0.33		ADENOSINE-5PHOSPHOSULFATE KINASE; CHAIN: A, B;	TRANSFERASE APS KINASE; APS KINASE, ADENYLYL SULFATE KINASE, SULFATE, NUCLEOTIDE 2 KINASE, TRANSFERASE
1048	1qf9	A	3	185	1.7e-21	0.34	0.99		URIDYL MONOPHOSPHATE/CYIDYL MONOPHOSPHATE KINASE; CHAIN: A; ₅	KINASE UMP/CMP KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE.
1048	1shk	A	1	186	1.7e-20	-0.06	0.84		SHIKIMATE KINASE; CHAIN: A, B;	PHOSPHORYL 2 TRANSFER, PHOSPHORYL 2 TRANSFER, TRANSITION STATE ANALOG COMPLEX, TRANSFERASE
1048	1ukz	6	185	1.4e-19	0.35	0.64		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-)	TRANSFERASE SHIKIMATE KINASE, PHOSPHORYL TRANSFER, ADP, SHIKIMATE 2 PATHWAY, P-LOOP PROTEIN, TRANSFERASE	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	PMF score	SEQFOIL D score	Compound	PDB annotation
1048	2cmk	A	6	187	1.7e-21	0.01	0.12	COMPLEXED WITH ADP AND AMP 1UKZ 3	
1048	3adk		3	184	8.5e-22	-0.02	0.22	CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE CK; NUCLEOTIDE MONOPHOSPHATE KINASE, TRANSFERASE
1049	1axi	B	162	349	1.7e-10	0.18	0.48	TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLYLATE KINASE (E.C.2.74.3) 3ADK 4	
1049	1bih	A	2	338	6.8e-21	0.21	-0.14	GROWTH HORMONE; CHAIN: A; GROWTH HORMONE RECEPTOR; CHAIN: B; HEMOLIN; CHAIN: A; B;	COMPLEX (HORMONE/RECEPTOR) HGH; HGHBP; COMPLEX (HORMONE/RECEPTOR)
1049	1bj8		253	350	1.9e-14	0.35	0.42	GP130; CHAIN: NULL;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1049	1bj8		360	461	3.8e-09	0.07	0.33	GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1049	1bj8							RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN	
1049	1bj8							RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN	
1049	1bj8							RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE,	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1049	1bp3	B	158	354	1.2e-21	0.14	0.05	GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B;	TITIN; CHAIN: NULL;	GLYCOPROTEIN HORMONE/GROWTH FACTOR HORMONE, RECEPTOR, HORMONE/GROWTH FACTOR CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bpv		159	259	3.8e-15	0.12	0.77			CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bpv		257	351	3.8e-12	0.59	0.30	TITIN; CHAIN: NULL;		CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bpv		479	572	5.1e-11	-0.02	0.25	TITIN; CHAIN: NULL;		CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bpv		479	578	9.5e-14	0.09	0.15	TITIN; CHAIN: NULL;		CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bpv		577	675	3.8e-17	0.28	0.55			CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bqu	A	158	363	8.5e-19	0.02	-0.09	GP130; CHAIN: A, B;		SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1049	1bqu	A	159	347	1.9e-20	-0.07	0.21	GP130; CHAIN: A, B;		SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1049	1bqu	A	256	479	3.8e-12	0.25	0.03	GP130; CHAIN: A, B;		SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1049	1bqu	A	358	581	1.7e-14	-0.05	0.10		GPI30; CHAIN: A; B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP 130, INTERLEUKINE 6 2, RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1049	1bqu	A	479	681	6.8e-23	0.04	0.09		GPI30; CHAIN: A; B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP 130, INTERLEUKINE 6 2, RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1049	1c8p	A	256	352	3.8e-13	0.36	0.35		CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN
1049	1c8p	A	359	457	7.6e-09	0.28	-0.12		CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN
1049	1cd9	B	159	356	9.5e-27	0.17	0.24		GRANULOCYTE COLONY-STIMULATING FACTOR; CHAIN: A; C; G-CSF RECEPTOR; CHAIN: B; D;	CYTOKINE G-CSF; G-CSF-R; CLASS I CYTOKINE, HEMATOPOIETIC RECEPTOR, SIGNAL TRANSDUCTION
1049	1cd9	B	360	564	7.6e-16	0.14	0.06		GRANULOCYTE COLONY-STIMULATING FACTOR; CHAIN: A; C; G-CSF RECEPTOR; CHAIN: B; D;	CYTOKINE G-CSF; G-CSF-R; CLASS I CYTOKINE, HEMATOPOIETIC RECEPTOR, SIGNAL TRANSDUCTION
1049	1cfb		156	350	1.1e-34	-0.07	0.55		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN	
									(CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) 1CFB 5	
1049	1cfb		255	456	1.9e-23	0.20	0.90		NEURAL ADHESION	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) 1CFB 5	
1049	1cfb								NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) 1CFB 5	
									NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) 1CFB 5	
									NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) 1CFB 5	
									NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) 1CFB 5	
1049	1cfb								NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) 1CFB 5	
1049	1cs6	A	272	671	6.8e-23	0.00	-0.20		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1049	1cs6	A	2	349	1.7e-35	0.15	-0.08		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1049	1cs6	A	350	750	3.4e-15	0.12	-0.17		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1049	1cs6	A	67	464	6.8e-30	-0.08	0.10		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFFOL D score	Compound	PDB annotation
1049	1cto		I57	247	7.6e-13	-0.16	0.04	GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1049	1cto		259	350	3.8e-13	0.12	0.09	GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1049	1cto		479	583	7.6e-10	0.47	-0.09	GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1049	1cvs	C	74	250	6.8e-31	0.25	0.42	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1cvs	D	2	135	1.5e-15	0.02	-0.15	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1cvs	D	61	153	5.7e-20	-0.01	0.19	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1cvs	D	74	250	1.7e-28	-0.03	0.51	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1eer	B	474	555	1.5e-07	0.08	0.13	ERYTHROPOETIN; CHAIN: A;	COMPLEX (CYTOKINE/RECEPTOR)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
								ERYTHROPOETIN RECEPTOR; CHAIN: B, C;	EPOBP; ERYTHROPOETIN, ERYTHROPOETIN RECEPTOR, SIGNAL 2 TRANSDUCTION, HEMATOPOIETIC CYTOKINE, CYTOKINE RECEPTOR 3 CLASS 1, COMPLEX (CYTOKINE/RECEPTOR) CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD,
1049	lepf	A	67	222	3.8e-14	0.02	0.27	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	GLYCOPROTEIN GLYCOPROTEIN
1049	lepf	A	71	234	6.8e-13	0.13	0.07	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD,
1049	lev2	E	74	250	1.7e-26	-0.02	0.65	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	lev2	G	74	254	3.4e-30	-0.14	0.12	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	levt	C	64	213	5.7e-20	-0.08	0.58	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	levt	C	74	250	1.7e-26	0.05	0.63	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN:	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1049	1f6f	B	160	354	3.4e-24	0.28	0.51		C, D;	SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	1f6f	B	70	253	1.7e-16	-0.23	0.03	PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4-HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
1049	1f6f	C	192	352	7.6e-10	-0.11	0.71	PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4-HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
1049	1fhg	A	475	572	5.1e-08	0.18	-0.20	TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL	
1049	1fna		486	565	1.7e-13	0.23	0.16	CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE II-10 IFNA 3	CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 IFNA 3	
1049	1fna		779	866	6.8e-09	0.38	-0.20	CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 IFNA 3	CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 IFNA 3	

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1049	1fmf		158	565	5.1e-36	0.25	0.98	FIBRONECTIN; CHAIN: NULL; IFNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
1049	1fmf		159	575	5.1e-36		166.16	FIBRONECTIN; CHAIN: NULL; IFNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
1049	1fmf		479	866	3.4e-33	0.29	0.23	FIBRONECTIN; CHAIN: NULL; IFNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
1049	1fmf		68	459	1.7e-26	0.24	0.76	FIBRONECTIN; CHAIN: NULL; IFNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
1049	1fmf		772	977	3.4e-12	0.08	-0.20	FIBRONECTIN; CHAIN: NULL; IFNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
1049	1fmh	A	272	564	1.7e-20	0.22	0.55	FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fmh	A	361	664	3.4e-27	0.26	0.07	FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fmh	A	482	751	3.4e-23	0.12	-0.07	FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fmh	A	580	855	8.5e-25	0.01	-0.19	FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fmh	A	70	333	1.4e-18	0.29	0.98	FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fmh	A	774	977	3.4e-20	0.05	-0.20	FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fmfn		157	343	1.1e-27	0.21	1.00	FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2
1049	1fmfn		162	343	3.4e-14	0.03	1.00	FIBRONECTIN; CHAIN: NULL;	HEPARIN-BINDING, GLYCOPROTEIN
1049	1fmfn		259	456	1.1e-20	-0.04	0.49	FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
										EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn		272	459	6.8e-11	0.13	0.45		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn	•	360	565	3.4e-20	0.05	0.13		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn		482	665	1.9e-27	0.24	0.17		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn		482	665	6.8e-25	0.20	-0.05		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	Inct		64	152	9.5e-23	0.16	1.00		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN
1049	1qg3	A	160	352	1.2e-15	0.19	0.99		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOLE	Compound	PDB Information
1049	1qg3	A	361	569	3.4e-19	0.11	0.59		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1049	1qg3	A	479	677	5.1e-26			103.51	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1049	1qg3	A	481	663	5.1e-26	0.23	0.43		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1049	1qg3	A	68	248	3.4e-17	0.29	0.66		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1049	1qr4	A	360	564	6.8e-12	0.24	0.43		TENASCIN CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-II, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1049	1qr4	A	711	862	3.4e-08	0.09	-0.20		TENASCIN CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-II, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1049	1qr4	A	776	971	3.4e-11	0.08	-0.20		TENASCIN CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-II, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1049	1tit		65	150	1.1e-19	0.70	0.15		TITIN, I27; CHAIN: NULL;	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN I27, TITIN IG REPEAT 27; MUSCLE PROTEIN.

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1049	1nm		67	152	1.9e-22	0.39	0.84		IMMUNOGLOBULIN-LIKE DOMAIN	
1049	1tff								IMMUNOGLOBULIN-TITIN MODULE M5 (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	
1049	1wif		776	866	1.7e-09	0.39	-0.20		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) ITTF 3	
1049	1wwc	A	65	152	1.9e-22	0.66	-0.09		MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN	
1049	2fcb	A	64	163	1.1e-21	0.18	0.59	NT-3 GROWTH FACTOR MODULE; CHAIN: NULL;	TWITCHIN 18TH LGSF TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D-DOMAIN SWAPPING, 2 TRANSFERASE	
1049	2fcb	A	60	251	9.5e-13	-0.00	0.01	FC GAMMA RIB, CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	
1049	2fib	A	154	250	1.5e-14	0.55	0.68	FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	
1049	2fib	A	255	345	9.5e-14	0.76	0.16	FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	
1049	2fib	A	359	465	9.5e-10	0.02	0.10	FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	
1049	2fib	A	475	570	1.9e-13	-0.12	0.04	FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
1049	2mb	A	574	670	1.5e-16	0.10	0.28		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPE III DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1049	3hfr	B	162	349	1e-10	0.16	0.13		HORMONE/RECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS RECEPTOR 3HHR 3 (EXTRACELLULAR DOMAIN) 3HHR 4	
1049	3hhc	B	162	351	3.8e-27	0.24	0.03		HORMONE/RECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS RECEPTOR 3HHR 3 (EXTRACELLULAR DOMAIN) 3HHR 4	
1049	3ncm	A	65	154	3.8e-23	0.45	0.46		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A _i	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1050	1bif	A	20	157	3.4e-29	0.09	-0.06		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1050	1cs6	A	4	158	3.4e-34	0.02	0.07		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1050	1cv5	C	3	157	3.4e-41	0.12	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN:	GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1050	1cv5	D	3	157	6.8e-42	0.22	0.33	C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1050	1epf	A	2	143	6.8e-22	-0.00	0.64	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;
1050	1ev2	E	3	157	1.7e-36	0.08	0.05	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;
1050	1ev2	E	90	162	8.5e-14	0.21	-0.05	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;
1050	1evt	C	3	157	1e-41	0.08	0.54	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;
1050	1t2q	A	2	162	1.7e-23	0.19	0.54	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1050	1fcg	A	2	159	8.5e-24	-0.02	0.90	FC RECEPTOR	IMMUNE SYSTEM, MEMBRANE

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
								FC(GAMMA)RIIA; CHAIN: A;	PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1050	1fng	A	1	75	1.2e-12	-0.10	0.63	TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1050	1fhg	A	76	157	3.4e-17	0.37	-0.14	TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1050	1fh1	A	2	147	1.9e-20	0.00	0.31	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A; TITIN; CHAIN: NULL;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1050	1nct		2	75	1.2e-12	0.07	0.87		MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1050	1nct		80	158	1.7e-16	0.20	-0.09	TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1050	1tmm		2	75	1.2e-12	0.43	0.54		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58
1050	1tmm		80	158	1.7e-16	0.07	-0.12		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED)

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOLE score	Compound	PDB annotation
1050	2dli	A	2	146	1.9e-19	-0.26	0.09	AVERAGE STRUCTURE) ITNM 4 ITNM 58	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1050	2fc6	A	2	160	6.8e-25	0.14	0.69	FC GAMMA RII; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1051	1aln	A	26	115	3.4e-43	-0.16	0.30	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF COMPLEX (ANTIGEN/PEPTIDE)
1051	1agd	A	26	115	3.4e-43	0.06	0.25	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8, B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1051	1duz	A	26	115	1.7e-42	0.18	0.22	HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1051	1efx	A	26	115	5.1e-43	0.24	0.28	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1051	1hoc	A	26	116	1.4e-42	0.34	0.69	HISTOCOMPATIBILITY ANTIGEN MURINE CLASS I	

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
									MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING 1HOC ₃ OF H-2D-B-, B2-MICROGLOBULIN, AND A 9-RESIDUE PEPTIDE 1HOC ₄	
1051	1hsb	A	26	115	8.5e-44	0.08	0.40		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN A W68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1051	1mhe	A	26	115	8.5e-43	0.13	0.25		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA-E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA-2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1051	1osz	A	26	115	1.2e-43	0.13	0.37		MHC CLASS I H-2KB HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; VESICULAR STOMATITIS VIRUS NUCLEOPROTEIN; CHAIN: C;	COMPLEX (MHC I/PEPTIDE) VSV-8; MHC/PEPTIDE COMPLEX, TRANSMEMBRANE PROTEIN, THYMIC 2 SELECTION, COMPLEX (MHC II/PEPTIDE)
1051	1qo3	A	26	115	3.4e-42	0.10	0.39		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49,

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1051	1tmc	A	26	115	8.5e-44	0.43	0.52		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A-W68 1TMc 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPPEYHRK) 1TMc 4	LY-49
1068	1mey	C	568	650	3.4e-49		100.26	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	
1068	1tf6	A	596	762	8.5e-38		108.39	TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	
1068	2gli	A	327	466	3.4e-34		89.55	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA, CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	
1070	1a25	A	160	291	5.1e-37		68.22	PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM+-+PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN	
1070	1rsy		154	283	3.4e-44		97.42	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2	•	

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOLED score	Compound	PDB annotation
1075	Igot	B	1	322	5.1e-89		116.65	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETERO TRIMER 2 SIGNAL TRANSDUCTION
1078	Igot	B	3	345	5.1e-81		104.69	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETERO TRIMER 2 SIGNAL TRANSDUCTION
1084	Imey	C	330	412	1.4e-48		107.26	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1084	1tf6	A	750	913	1e-37		114.17	TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1084	2gli	A	302	441	1.4e-33		103.60	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOIL D score	Compound	PDB annotation
										GII, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1090	1evh	A	9	122	3.4e-50		82.80		MENA EVH1 DOMAIN; CHAIN: A; PEPTIDE ACTA; CHAIN: B;	CONTRACTILE PROTEIN WH1 DOMAIN; MOLECULAR RECOGNITION, ACTIN DYNAMICS, CONTRACTILE PROTEIN
1090	1qc6	A	9	121	1.7e-44		62.71		EVH1 DOMAIN FROM ENAVASP-LIKE PROTEIN; CHAIN: A, B; PHE-GLU-PHE-PRO-PRO-PRO-THR-ASP-GLU-GLU; CHAIN: C, D;	CELL MOTILITY AN INCOMPLETE SEVEN STRANDED ANTI-PARALLEL BETTA BARREL 2 CLOSED BY AN ALPHA HELIX, EVH1 DOMAIN, ACTIN-BASED CELL 3 MOTILITY, INTERACTION MODULE
1095	1alk	A	391	473	1.7e-26		84.85		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, PROTEIN-DNA-BINDING PROTEIN
1095	1mey	C	418	500	1.4e-45		110.38		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1095	1tf6	A	362	530	3.4e-34		120.65		TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1095	1ubd	C	336	444	3.4e-33		98.51		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, YY1, ZINC 2 INITIATOR ELEMENT

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
1095	2gli	A	334	473	6.8e-34		105.76	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;		FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION, DNA)
1101	1edh	A	62	266	5.1e-48		122.19	E-CADHERIN; CHAIN: A; B;		COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1101	1ncj	A	61	265	6.8e-50		122.32	N-CADHERIN; CHAIN: A;		CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2; ECAD12; CADHERIN, CELL-ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1105	1aj4		72	237	8.5e-36		73.76	TROPONIN C; CHAIN: NULL;		CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1105	1au1	B	74	249	1.7e-39		92.24	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;		MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1105	1bjf	A	65	245	1.7e-49		184.52	NEUROCALCIN DELTA; CHAIN: A, B;		HYDROLASE CALCINEURIN, HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1105	1cdm	A	82	234	1.4e-55		57.84	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4		CALCIUM-BINDING PROTEIN 2 CYCLASE ACTIVATOR
1105	1cll		82	235	3.4e-60		67.88	CALCIUM-BINDING PROTEIN		

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1105	1iku		62	245	3.4e-39		160.57	CALMODULIN (VERTEBRATE) ICLL3 RECOVERIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCIUM-BINDING PROTEIN
1105	1rec		68	250	1.7e-34		143.82	CALCIUM-BINDING PROTEIN RECOVERIN (CALCIUM SENSOR IN VISION) IREC 3	
1105	1tcf		70	235	1.5e-39		73.38	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1105	1tnx		67	233	1e-38		69.96	TROPONIN C; 1TNX 4 CHAIN; NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
1105	1top		63	237	8.5e-40		73.36	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
1105	1vrik	A	79	236	3.4e-39		68.28	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1105	2scp	A	34	205	3.4e-09		53.97	BINDING PROTEIN SARCOPLASMIC CALCIUM-BINDING PROTEIN 2SCP 3	
1114	1am4	D	51	216	6.8e-48		70.86	P50-RHOGAP; CHAIN: A, B, C; CDC42HS; CHAIN: D, E, F;	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING) COMPLEX (GTPASE-ACTIVATING/GTP-BINDING), GTPASE ACTIVATION
1114	1byu	A	45	231	8.5e-52		74.78	GTP-BINDING PROTEIN RAN;	TRANSPORT PROTEIN TC4; GTPASE,

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
1114	1byu	B	41	231	1.7e-52			69.65	CHAIN: A; B; GTP-BINDING PROTEIN RAN; CHAIN: A, B;	NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1114	1cly	A	50	216	1.7e-63			67.97	RAS RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONCOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1114	1ctq	A	50	217	1.7e-62			75.99	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1114	1czx	A	47	222	1.5e-54			82.44	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B;	SIGNALING PROTEIN PROTEIN-PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL
1114	1hur	A	37	218	5.1e-12			71.40	HUMAN ADP-RIBOSYLATION FACTOR 1; IHUR 5 CHAIN: A, B; IHUR 7	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED 1HUR 16
1114	1ibr	A	52	221	3.4e-51			86.05	RAN CHAIN: A; IMPORTIN BETA SUBUNIT; CHAIN: B; D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1114	1kao		50	217	3.4e-60			79.99	RAP2A; CHAIN: NULL;	GTP-BINDING PROTEIN GTP-BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS
1114	1mh1		49	222	1.2e-54			77.42	RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
1114	1np	C	47	231	3.4e-51			89.47	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOLE score	Compound	PDB annotation
1114	1ex4	B	51	216	1.4e-51		70.72	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: E;	TRANSPORT COMPLEX(GTPASE ACTIVATIN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2, TRANSITION STATE, GAP COMPLEX (GTP- BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP- BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1114	1zbd	A	49	226	1.7e-63		93.30	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	
1114	2ngr	A	50	230	3.4e-50		77.06	GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3, HYDROLASE
1114	3rab	A	47	221	6.8e-65		102.45	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1116	2bnh		2	324	1.7e-52		56.47	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE, PROTEIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1120	5pnt		2	140	1.4e-54		214.70	LOW MOLECULAR WEIGHT PHOSPHOTYROSYL PHOSPHATASE; CHAIN: NULL;	HYDROLASE ORTHOPHOSPHORIC MONOESTER PHOSPHOHYDROLASE; HYDROLASE, ACETYLATION, TYROSINE PHOSPHATASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1122	lav1	A	83	280	5.1e-05		51.65	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2, ATHEROSCLEROSIS, HDL, LCAT- ACTIVATION
1127	1a01	A	465	741	3.4e-76		100.75	BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1127	1a5i	A	454	739	5.1e-67		106.52	PLASMINOGEN ACTIVATOR; CHAIN: A; GLU-GLY-ARG CHLOROMETHYL KETONE; CHAIN: I;	COMPLEX (SERINE PROTEASE/INHIBITOR) (DELTAFEK)DSPALPHAI; EGRCMK; SERINE PROTEASE, FIBRINOLYTIC ENZYMES, PLASMINOGEN 2 ACTIVATORS
1127	1aht	H	465	744	1.5e-73		91.53	ALPHA-THROMBIN; 1AHT 4 CHAIN: L, H; 1AHT 5 HIRUGEN; 1AHT 8 CHAIN: I; 1AHT 9	COMPLEX (SERINE PROTEINASE/INHIBITOR)
1127	laut	C	464	739	5.1e-68		99.33	ACTIVATED PROTEIN C; CHAIN: C; L-D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN II A; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1127	1ekb	B	468	739	1.7e-76		89.82	ENTEROPEPTIDASE; CHAIN: A; ENTEROPEPTIDASE; CHAIN: B; VAL-ASP-ASP-ASP-ASP-LYS PEPTIDE; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END A A	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1127	1et	H	465	745	1.5e-71		92.09	HYDROLASE(SERINE PROTEINASE) EPSILON-THROMBIN (E.C.3.4.21.5) NON-COVALENT COMPLEX WITH IETR3 MQPA IETR 4	
1127	1fky	A	463	742	1.4e-76		89.40	COAGULATION FACTOR XA-TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG-CHLOROMETHYLKETONE (PPACK) WITH CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACK, 2 CHLOROMETHYLKETONE,
1127	1kig	H	465	745	3.4e-70		98.96	FACTOR XA; CHAIN: H, L; ANTIKOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RIAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1127	1mkx	K	425	739	1.7e-72		93.49	ALPHA-THROMBIN; CHAIN: L; H; PRETHROMBIN-2; CHAIN: K;	COMPLEX (BLOOD COAGULATION/PROENZYME)
1127	1pyt	D	454	739	1.5e-75		95.69	PROCARBOXYPEPTIDASE A; CHAIN: A, B; PROPROTEINASE E; CHAIN: C; CHYMOTRYPSINOGEN C; CHAIN: D;	TERNARY COMPLEX (ZYMOGEN) TC, PCPA-Tc; TERNARY COMPLEX (ZYMOGEN), SERINE PROTEINASE, C-TERMINAL 2 PEPTIDASE
1127	1rf	B	467	740	1.7e-68		102.89	TWO CHAIN TISSUE PLASMINOGEN ACTIVATOR; CHAIN: A, B;	SERINE PROTEASE (TC)-T-PA; SERINE PROTEASE, FIBRINOLYTIC ENZYMES
1135	1mey	C	342	430	6.8e-47		71.69	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFFOL D score	Compound	PDB annotation
1135	1tf3	A	342	433	1.5e-21			67.88	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	(ZINC FINGER/DNA)
1135	1tf6	A	276	454	3.4e-41			105.09	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA); RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1135	lubd	C	277	400	1.7e-30			80.44	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YY1-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1135	2gli	A	277	431	1.4e-60			202.77	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA, CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1139	1mab	B	1	183	1.7e-46			64.40	F1-ATPASE ALPHA CHAIN; CHAIN: A; F1-ATPASE BETA CHAIN; CHAIN: B; F1-ATPASE GAMMA CHAIN; CHAIN: G;	HYDROLASE ATP SYNTHASE, FOF1- ATPASE, OXIDATIVE PHOSPHORYLATION, 2 MITOCHONDRIA, HYDROLASE

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	PMF score	SEQFFOL D score	Compound	PDB annotation
1140	1mab	B	51	264	6.8e-66			130.11	HYDROLASE ATP SYNTHASE, FOF1-ATPASE, OXIDATIVE PHOSPHORYLATION, 2 MITOCHONDRIA, HYDROLASE
1148	1crz	A	3	122	1.6e-09	0.19	0.17	TOLB PROTEIN, CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS; BETA PROPELLER AND ALPHA/BETA FOLD
1148	1ejj	A	11	127	3.2e-29	0.70	0.94	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1148	1ejj	A	3	79	3.2e-10	0.16	0.18	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1148	1got	B	6	122	8e-22	0.01	0.40	GT-ALPHA/GL-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER) G PROTEIN, HETERO TRIMER 2 SIGNAL TRANSDUCTION
1149	1efl	A	43	326	1.4e-97	0.69	1.00	MOESIN; CHAIN: A, B; MOESIN; CHAIN: C, D;	MEMBRANE PROTEIN CRYSTAL STRUCTURE, MEMBRANE, FERM DOMAIN, TAIL DOMAIN
1153	1a06	36	339	0				329.67	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;
1153	1a06	6	334	0		0.64	1.00	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFFOL D score	Compound	PDB annotation
1155	1cf6		51	203	1e-28			82.01	PATHOGENESIS-RELATED PROTEIN PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1 PROTEINS, 2 PLANT DEFENSE
1155	1cf6		52	203	1e-28	0.47	1.00		PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1 PROTEINS, 2 PLANT DEFENSE
1156	1ds6	A	1	96	1.2e-46	0.06	1.00		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISASSOCIATION INHIBITOR 2; CHAIN: B;	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SAND WHICH PROTEIN-PROTEIN COMPLEX, G-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING PROTEIN
1159	1qf9	A	23	239	1.5e-19	-0.03	0.62		URIDYLMONOPHOSPHATE/CY TIDYLMONOPHOSPHATE KINASE; CHAIN: A;	KINASE UMP/CMP KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE, PHOSPHORYL 2 TRANSFER, TRANSITION STATE ANALOG COMPLEX, TRANSFERASE TRANSFERASE TRANSFERASE TRANSFERASE
1159	1qhf	A	249	424	5.1e-47	0.47	1.00		PHOSPHOGLYCERATE MUTASE; CHAIN: A; B; PHOSPHOGLYCERATE MUTASE; CHAIN: A; B;	(PHOSPHORYL) (PHOSPHORYL) TRANSFERASE TRANSFERASE (PHOSPHORYL)
1159	3adk		36	236	3.4e-26	-0.17	0.68		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.74.3) 3ADK 4	

SEQ ID NO:	PDB ID	CHAI NID	STAR T AA	END AA	Psi Blast score	PMF score	SEQFOL D score	Compound	PDB annotation
1159	3pgm	249	441	1.7e-48	0.19	1.00		TRANSFERASE (PHOSPHORYL) PHOSPHOGLYCERATE MUTASE (E.C.2.7.5.3) DE-PHOSPHO ENZYME 3PGM 4	
1159	3pgm	249	441	1.7e-48			58.96	TRANSFERASE (PHOSPHORYL) PHOSPHOGLYCERATE MUTASE (E.C.2.7.5.3) DE-PHOSPHO ENZYME 3PGM 4	
1159	3trmk	A	34	237	1.2e-29	-0.13	0.19	THYMIDYLATE KINASE; CHAIN: A, B, C, D, E, F, G, H;	KINASE KINASE, PHOSPHOTRANSFERASE
1160	Imey	C	360	442	4.8e-51			DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1160	1ff6	A	276	437	8e-38		108.88	TFIIA; CHAIN: A; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1160	lubd	C	334	442	5.1e-53		86.63	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YY1-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1160	2gji	A	304	443	3.2e-34		98.31	ZINC-FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1163	1a06									BINDING PROTEIN/DNA)
1163	1a60		43	340	3.2e-84			130.42	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1163	1a60		18	334	6.8e-54			108.45	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1163	1apm	E	18	353	0			168.88	TRANSFERASE (PHOSPHOTRANSFERASE) SC-AMP'S-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (SC/APPK\$) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6 CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	• • •
1163	1aq1		50	348	4.8e-56			111.26		PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAURSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1163	1b18	A	51	323	6.8e-56			93.00	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1163	1bix	A	47	331	6.8e-62			113.75	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:	COMPLEX (INHIBITOR PROTEINKINASE) INHIBITOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
		*						B;	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1163	1byg	A	44	300	1.3e-31		93.49	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE
1163	1cmk	E	9	353	0		175.36	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1163	1ctp	E	15	343	0		168.10	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1163	1fgk	A	39	309	6.4e-31		106.44	FGF RECEPTOR 1; CHAIN: A; B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1163	1fgk	B	36	304	1.3e-37		117.87	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1163	1hcl	50	348	1e-66			128.78	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
1163	1ir3	A	38	323	3.2e-26				INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1163	1jnk						99.07		C-TUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; SERINE/THREONINE PROTEIN 2 KINASE
1163	1kob	A	24	359	1e-90				TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1163	1p38		31	395	1.6e-50		109.88		MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1163	1phk		49	305	1.1e-83			156.26	PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1163	1pmc							104.21	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1163	1tkd	A	47	370	8e-57			131.84	TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
1163	3erk		36	400	3.4e-69			116.38	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TITIN, MUSCLE, AUTOINHIBITION TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1170	1bw_m	A	17	247	1.6e-12			50.07	ALPHA-BETA T CELL RECEPTOR (TCR) (D10); CHAIN: A;	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNORECEPTOR, IMMUNE SYSTEM
1170	1cdy		22	190	0.00034			50.90	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1170	1f58	H	17	244	4.8e-21			51.50	IGG1 ANTIBODY 58.2 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 58.2 (HEAVY CHAIN); CHAIN: H; EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); CHAIN: P;	IMMUNE SYSTEM FAB 58.2; FAB 58.2; V3 LOOP; IMMUNOGLOBULIN, FAB, HIV-1, GP120, V3, IMMUNE SYSTEM
1170	1fg	H	17	239	8e-19			51.43	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (KAPPA LIGHT CHAIN) FAB' FRAGMENT 1 FIG 3	
1170	1qrn	D	14	219	6.4e-23			50.17	MHC CLASS IHL-A; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE P6A; CHAIN: C; HMAN T-CELL RECEPTOR; CHAIN: D; HLA-A 0201; CHAIN: E;	IMMUNE SYSTEM HUMAN TCR/PEPTIDE/MHC COMPLEX, HLA- A2, HTLV-1, TAX, TCR, T 2 CELL RECEPTOR, IMMUNE SYSTEM

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOLD score	Compound	PDB annotation
1170	2fgb	A	15	240	1.6e-17			51.08	IMMUNOGLOBULIN IGG2A FAB FRAGMENT (CNJ206) 2GFB 3	
1170	2gcp	B	17	239	9.6e-21			51.13	IMMUNOGLOBULIN; CHAIN: A, B, C, D;	IMMUNOGLOBULIN
1174	1ai7		152	245	0.0017	-0.20	0.04	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL,	HYDROLASE TETRATICOPEPTIDE-TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	
1180	1fib		195	418	1.7e-53			129.15	GAMMA-FIBRINOGEN CARBOXYL TERMINAL FRAGMENT; CHAIN: NULL;	BLOOD COAGULATION FACTOR BLOOD COAGULATION, GLYCOPROTEIN, CALCIUM, PLATELET, PLASMA, 2 ALTERNATIVE SPLICING SIGNAL, DISEASE MUTATION, POLYMORPHISM
1180	1fzc	B	148	416	1.7e-63			132.32	FIBRIN; CHAIN: A, B, C, D, E, F, G, H, I, J;	BLOOD COAGULATION BLOOD COAGULATION, PLASMA PROTEIN, CROSSLINKING
1180	1fzc	C	151	422	3.4e-62			141.90	FIBRIN; CHAIN: A, B, C, D, E, F, G, H, I, J;	BLOOD COAGULATION BLOOD COAGULATION, PLASMA PROTEIN, CROSSLINKING
1180	1fzd	A	242	419	1.7e-57			154.36	FIBRINOGEN-420; CHAIN: A, B, C, D, E, F, G, H;	BLOOD COAGULATION BLOOD COAGULATION, FIBRINOGEN-420, ALPHAEC DOMAIN, 2 FIBRINOGEN RELATED DOMAIN, GLYCOSYLATED PROTEIN
1180	1fzg	C	170	419	1.1e-39			141.24	FIBRINOGEN; CHAIN: A, B, C, D, E, F, S, T, M, N;	BLOOD COAGULATION BLOOD COAGULATION, PLASMA, PLATELET, FIBRINOGEN, FIBRIN
1180	1fzg	E	160	416	3.2e-39			130.27	FIBRINOGEN; CHAIN: A, B, C,	BLOOD COAGULATION BLOOD

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
									D, E, F, S, T, M, N;	COAGULATION, PLASMA, PLATELET, FIBRINogen, FIBRIN
1181	1fim		2	104	1.6e-43		145.02		MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: NULL;	CYTOKINE MACROPHAGE, INFLAMMATORY RESPONSE, CYTOKINE
1181	1gif	A	1	115	1.6e-52		180.54		GLYCOSYLATION-INHIBITING FACTOR; CHAIN: A, B, C;	CYTOKINE MACROPHAGE, INFLAMMATORY RESPONSE, CYTOKINE
1181	1mfi	A	2	115	3.2e-52		170.94		MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: A, B, C;	CYTOKINE PHENYLpyruVATE TAUTOMERASE, CYTOKINE, MACROPHAGE, INFLAMMATORY RESPONSE, TAUTOMERASE
1185	1d2n	A	195	450	1.2e-35		76.43		N-ETHYLMaleIMIDE-SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN HEXAMERIZATION DOMAIN, ATPase, TRANSPORT
1195	1a8y		382	723	4.8e-25		91.59		CALSEQUESTRIN; CHAIN: NULL	CALCIUM-BINDING PROTEIN CALSEQUESTRIN, CALCIUM-BINDING PROTEIN, SARCOPLASMIC 2 RETICULUM, RABBIT SKELETAL MUSCLE
1200	1ayz	A	31	190	3.2e-47		71.29		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
1200	1c4z	D	47	191	9.6e-40		84.49		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C;	LIGASE E6AP, UBC7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2, 2
1200	1qcq	A	44	193	3.2e-53		81.61		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	UBIQUITIN CONJUGATING ENZYME, YEAST

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1200	1u9a	A	24	193	1.6e-43		74.19	UBC9; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME UBIQUITIN CONJUGATING ENZYME; UBIQUITIN CONJUGATING ENZYME; UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
1200	2aaK		31	193	3.2e-47		71.32	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, LIGASE
1200	2e2c		26	193	1.4e-41		67.54	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
1200	2aoz		33	193	3.2e-43		64.54	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7, UBIQUITIN CONJUGATION, LIGASE, YEAST
1204	1awj		241	317	3.2e-15	-0.35	0.06	ITK; CHAIN: NULL;	TRANSFERASE IL-2-INDUCIBLE T-CELL KINASE, TRANSFERASE, REGULATOR INTRAMOLECULAR COMPLEX, KINASE
1204	1aww		250	319	1.1e-13	0.55	0.58	BRUTON'S TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE ATK, AMGX1, BPK; TYROSINE KINASE, X-LINKED AGAMMAGLOBULINEMIA, XLA, BTK, SH3 2 DOMAIN, TRANSFERASE
1204	1bu1	A	258	318	4.8e-15	0.03	0.21	HEMPOOETIC CELL KINASE; CHAIN: A, B, C, D, E, F;	TRANSFERASE TYROSINE-PROTEIN KINASE, TRANSFERASE, SIGNAL TRANSDUCTION, 2 SH3
1204	1efh	A	258	317	1.6e-17	0.12	0.82	FYN TYROSINE KINASE; CHAIN: A, C; HTV-1 NEF PROTEIN; CHAIN: B, D;	COMPLEX (SH3 DOMAIN)VIRAL ENHANCER) SRC-HOMOLOGY 3 DOMAIN; COMPLEX (SH3 DOMAIN)VIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL	Compound	PDB annotation
										PROTEIN KINASE, PHOSPHORYLATION, 3' AIDS, MYRISTYLATION, GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPI HELIX, PXXP MOTIF
1204	1fyn	A	255	318	6.4e-19	0.32	0.58	PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;		TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO- ONCOGENE, TRANSFERASE, PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1204	1gbr	A	260	322	4.8e-12	0.25	0.63	SIGNAL TRANDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5		
1204	1ln6	C	259	316	1.3e-16	0.42	0.69	C-SRC; CHAIN: C; NLI (MN7- MN2-MN1-PLPPPLP); CHAIN: N;		COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PEPTIDE)
1204	1qly	A	257	318	4.8e-13	0.41	0.43	TYROSINE-PROTEIN KINASE BTK; CHAIN: A;		TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE- PROTEIN KINASE PHOSPHORYLATION, 2 SH3 DOMAIN
1204	1shf	A	256	318	8e-19	0.39	0.31	PHOSPHOTRANSFERASE FYN		

SEQ NO:	PDB ID	CHAI NID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
									PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.11.2) 1SHF3 (SH3 DOMAIN) 1SHF4	
1204	2abi		251	423	9.6e-28	0.04	-0.15		ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN
1204	4hck		255	318	3.2e-15	0.04	0.55		HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	TRANSFERASE HCK; SH3 PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
1205	1cxy	A	38	98	0.0096	0.69	0.19		CYTOCHROME B5; CHAIN: A;	ELECTRON TRANSPORT HELIX, BETA-STRAND, ELECTRON TRANSPORT
1208	1cho	I	554	592	5.1e-07	-0.30	0.58		COMPLEX(SERINE PROTEINASE-INHIBITOR) ALPHA-CHYMOTRYPSIN (E.C.3.4.21.1) COMPLEX WITH TURKEY 1CHO4 OYOMUCOID THIRD DOMAIN (/OMTKY3\$) 1CHO 5	
1208	1ldt	L	559	587	1.7e-07	-0.23	0.86		TRYPSIN; CHAIN: T; TRYPTASE INHIBITOR; CHAIN: L;	COMPLEX (HYDROLASE/INHIBITOR) LD1; COMPLEX (HYDROLASE/INHIBITOR), HYDROLASE, INHIBITOR, 2 INFLAMMATION, TRYPTASE
1215	1ak8								CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN CERUM TRIC- DOMAIN, RESIDUES 1 - 75; CERUM-LOADED, CALCIUM-BINDING PROTEIN
1215	1c7w	A	349	410	6.8e-06	-0.50	0.23		CALCIUM VECTOR PROTEIN;	METAL BINDING PROTEIN CAVP;

SEQ ID NO:	PDB ID	CHAIN NID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOIL D score	Compound	PDB annotation
1215	1cdm	A	356	418	3.4e-05	-0.48	0.09		CHAIN: A;	EF-HAND FAMILY, CALCIUM BINDING PROTEIN, NMR
1215	1cho	I	39	84	5.1e-10	0.04	0.65		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM ³ CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4 COMPLEX(SERINE PROTEINASE-INHIBITOR) ALPHA-CHYMOTRYPSIN (E.C.3.4.21.1) COMPLEX WITH TURKEY 1CHO 4 OVOMUCOID THIRD DOMAIN (/OMTKY3\$) 1CHO 5	
1215	1dfl	A	349	410	1.7e-05	-0.26	0.21		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX- TURN-HELIX
1215	1exr	A	348	414	1.4e-05	0.15	0.05		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN
1215	1ezg	A	226	305	3.2e-06	0.21	0.13		THERMAL HYSTERESIS PROTEIN ISOFORM YL-1; CHAIN: A, B;	HIGH RESOLUTION DISORDER ANTIFREEZE PROTEIN INSECT HYSTERESIS, TENEBRIOS 2 MOUTOR, IODINATION, RIGHT-HANDED BETA-HELIX, TMAPP
1215	1f71	A	349	410	6.8e-05	0.10	0.69		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
1215	1fak	L	236	302	4.8e-09	0.07	-0.19		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; SL15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOLE D score	Compound	PDB annotation
1215	1nub	A	201	426	1.7e-28			73.86	BASEMENT MEMBRANE PROTEIN BM-40; CHAIN: A, B;	PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
1215	1qjt	A	348	419	6.8e-07	-0.05	0.01		EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CHAIN: A;	GROWTH FACTOR EHI; EH DOMAIN, EPS15, EF-HAND, SOLUTION STRUCTURE, S100 PROTEIN
1215	1rro		348	410	3.4e-05	-0.37	0.19		CALCIUM-BINDING PROTEIN RAT ONCOMODULIN 1RRO_3	
1215	1sgp	I	43	84	1.7e-08	0.67	0.55		STREPTOMYCES GRISEUS PROTEINASE B; 1SGP 6 CHAIN: E; 1SGP 7 TURKEY OVOUMUCOID INHIBITOR; 1SGP 11 CHAIN: I; 1SGP 12 SPARC; 1SRA 4 CHAIN: NULL; 1SRA 5	COMPLEX (SERINE PROTEASE/INHIBITOR) SGPB; 1SGP 8 ALA18-OMTKY3; 1SGP 14 SERINE PROTEINASE, PROTEIN INHIBITOR 1SGP 25
1215	1sra		279	423	1.5e-38	0.43	0.72		CALCIUM-BINDING PROTEIN BM-40, OSTEONECTIN; 1SRA 7 EXTRACELLULAR MATRIX PROTEIN 1SRA 20	
1215	1sra		279	426	1.5e-38			58.51	SPARC; 1SRA 4 CHAIN: NULL; 1SRA 5	CALCIUM-BINDING PROTEIN BM-40, OSTEONECTIN; 1SRA 7 EXTRACELLULAR MATRIX PROTEIN 1SRA 20
1215	1xka	L	240	313	4.8e-09	0.09	-0.19		BLOOD COAGULATION FACTOR XA; CHAIN: L, C,	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMR D score	SEQFOL D score	Compound	PDB annotation
1215	3ovo		40	84	1.7e-09	0.76	0.21			GROWTH FACTOR LIKE DOMAIN
1215	5pal		348	410	3.4e-05	-0.11	0.13		PROTEINASE INHIBITOR (KAZAL) OVOMUCOID THIRD DOMAIN CLEAVED RDI3OVO 3	
1215	9wga	A	112	286	3.2e-15	0.08	-0.19		CALCIUM-BINDING PROTEIN PARVALBUMIN (ALPHA LINEAGE) SPAL 3	
1216	1a8a		1	217	3.2e-51	0.58	1.00		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1216	1a8a		1	217	3.2e-51				ANNEXIN V; CHAIN: NULL; PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN	
1216	1ain		61	222	1e-68	0.23	1.00	75.48	ANNEXIN V; CHAIN: NULL; PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN	
1216	1ain		61	223	1e-68				CALCIUM/PHOSPHOLIPID BINDING ANNEXIN 1A1N 3	
1216	1ain		62	222	4.8e-67	-0.02	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN 1A1N 3	
1216	1ala		1	214	3.2e-53	0.42	1.00		CALCIUM/PHOSPHOLIPID- BINDING PROTEIN ANNEXIN V 1ALA 3	
1216	1ala		1	214	3.2e-53			75.25	CALCIUM/PHOSPHOLIPID- BINDING PROTEIN ANNEXIN V 1ALA 3	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOLD score	Compound	PDB annotation
1216	1ann	11	215	9.6e-51	0.42	1.00			ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12.2 CHROMOBINDIN IV, PROTEIN II 1ANN 13
1216	1ann	1	216	3.2e-67			68.51		ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12.2 CHROMOBINDIN IV, PROTEIN II 1ANN 13
1216	1ann	62	219	3.2e-67	0.46	1.00			ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12.2 CHROMOBINDIN IV, PROTEIN II 1ANN 13
1216	1avc	10	216	1.6e-50	0.24	1.00			ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN
1216	1avc	5	221	9.6e-78	0.48	1.00			ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1216	Iaxn	4	216	9.6e-53	0.76	1.00			ANNEXIN III; IAXN 4 CHAIN: NULL; IAXN 5	PROTEIN CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1216	Iaxn	53	223	3.2e-67			84.90		ANNEXIN III; IAXN 4 CHAIN: NULL; IAXN 5	PROTEIN CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1216	Iaxn	59	222	3.2e-67	0.70	1.00			ANNEXIN III; IAXN 4 CHAIN: NULL; IAXN 5	PROTEIN CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1216	Ihvd	1	212	1.1e-49			69.28		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V CLIPOCORTIN V, ENDONEXIN II, PLACENTAL 1HVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION 1HVD 4 WITH GLU 117 REPLACED BY GLY (E17G) 1HVD 5	
1217	Ia8a	8	189	8e-39	0.64	1.00			ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN: PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1217	Iain	13	187	8e-32	0.22	1.00			CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I1AIN 3	
1217	Iain	33	304	0			403.43		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I1AIN 3	
1217	Iain	35	300	0	0.17	1.00			CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I1AIN 3	
1217	Iala	8	186	3.2e-38	0.31	1.00			CALCIUM/PHOSPHOLIPID- BINDING PROTEIN ANNEXIN V 1ALA 3	

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOLD D score	Compound	PDB annotation
1217	Iann	8	187	3.2e-38	0.55	1.00			ANNEXIN IV; IANN 5 CHAIN: NULL; IANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I, IANN 1, IANN 2, KBD CALLELECTRIN, ENDONEXIN I, IANN 1, IANN 2, LPOCORTIN, ENDONEXIN I, LPOCORTIN IV, IANN 12.2 CHROMOBINDIN IV, PROTEIN II IANN 13
1217	1avc	8	186	4.8e-26	0.28	1.00			ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN
1217	laxn	8	187	1.6e-37	0.54	1.00			ANNEXIN III; IAXN 4 CHAIN: NULL; IAXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY IAXN 14
1217	1hvd	8	184	6.4e-38	0.31	1.00			CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V, ENDONEXIN II, PLACENTAL IHVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION IHVD 4 WITH GLU 17 REPLACED BY GLY (E17G) IHVD 5	
1218	1a8a	31	195	3.2e-66			58.84		ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1218	1a8a	33	194	3.2e-66	0.68	1.00			ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOLE	Compound	PDB annotation
										PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1218	1ain	33	194	1e-68	0.23	1.00			CALCIUM/PHOSPHOLIPID	
1218	1ain	33	195	1e-68			170.39		BINDING ANNEXIN I IAIN 3	
1218	1ain	35	194	1.6e-65	0.15	1.00			CALCIUM/PHOSPHOLIPID	
1218	1ann	33	195	3.2e-68			65.05		BINDING ANNEXIN I IAIN 3	
									ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	
										CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12.2 CHROMOBINDIN IV, PROTEIN II IANN 13
1218	1ann	34	190	3.2e-68	0.54	1.00			ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	
										CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12.2 CHROMOBINDIN IV, PROTEIN II IANN 13
1218	1avc	2	186	1.6e-38	0.30	1.00			ANNEXIN VI; CHAIN: NULL;	
										CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN
1218	1avc	34	193	1.6e-71	0.61	1.00			ANNEXIN VI; CHAIN: NULL;	
										CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOLE D score	Compound	PDB annotation
1218	1axn			25	195	6.4e-67				MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN
1218	1axn			31	194	6.4e-67	0.70	85.90	ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1218	1dk5	A		2	169	3.2e-19	0.02	1.00	ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1218	1hv4			32	195	9.6e-68			ANNEXIN 24(CA32); CHAIN A, B;	METAL BINDING PROTEIN PLANT ANNEXIN, CAPSICUM ANNUUM, BELL PEPPER, CALCIUM 2 BINDING PROTEIN
1218	1hv4			33	194	9.6e-68	0.59	68.02	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V, ENDONEXIN II, PLACENTAL IHVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION IHVD 4 WITH GLU 17 REPLACED BY GLY (E17G) IHVD 5	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V, ENDONEXIN II, PLACENTAL IHVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION IHVD 4 WITH GLU 17 REPLACED BY GLY (E17G) IHVD 5
1219	1b3u	A		23	627	1.6e-45			PROTEIN PHOSPHATASE PP2A; CHAIN A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOLE	Compound	PDB annotation
1219	1b3u	A	320	643	1.6e-09	0.07	0.23		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	PHOSPHORYLATION, HEAT REPEAT SCAFFOLD PROTEIN SCAFFOLD
1219	1b3u	A	71	625	1.6e-45	0.04	-0.07		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A,
1219	1ee4	A	211	473	1.7e-10	0.36	1.00		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	PHOSPHORYLATION, HEAT REPEAT TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1219	1ee4	A	279	643	1.4e-44	0.57	0.86		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1219	1i1l	A	179	628	1.3e-43			118.96	IMPORTIN ALPHA; CHAIN: A; IMPORTIN ALPHA; CHAIN: B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
1219	1i1l	A	272	643	1.3e-43	0.50	0.53		IMPORTIN ALPHA; CHAIN: A; IMPORTIN ALPHA; CHAIN: B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
1219	1ibr	B	318	633	4.8e-15	0.01	-0.15		RAN _Q CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GIPASE KARYOPHERIN BETA, P95 SMALL GIPASE, NUCLEAR TRANSPORT RECEPTOR
1219	2bct		239	643	1.1e-39	0.51	0.06		BETA-CATENIN; CHAIN: NULL;	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA.

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOLE score	Compound	PDB annotation
1219	3bct		277	643	3.2e-35	0.46	0.24		BETA-CATENIN; CHAIN: NULL;	CATENIN, STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
1221	1bu7	A	19	486	9.6e-53			174.17	CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK OXIDOREDUCTASE (OXYGENASE)
1221	1oxa		27	486	3.2e-24			94.76	CYTOCHROME P450 ERYF; 1OXA_5 CHAIN: NULL 1OXA_6	
1222	1bu7	A	35	324	1.3e-18	-0.20	0.04		CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1222	1bu7	A	61	318	3.4e-36	-0.23	0.29		CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1222	1dt6	A	31	325	3.2e-92	-0.02	0.99		CYTOCHROME P450 2C5; CHAIN: A;	OXIDOREDUCTASE PROGESTERONE 21-HYDROXYLASE, CYPIC5 P450 1, MEMBRANE PROTEIN, PROGESTERONE 21-HYDROXYLASE, BENZO(A) 2 PYRENE HYDROXYLASE, ESTRADIOL 2-HYDROXYLASE, P450, CYP2C5
1222	1f26	A	48	318	1.7e-21	-0.08	0.05		NITRIC OXIDE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE NITRIC OXIDE REDUCTASE, CYTOCHROME P450NOR
1222	1oxa		61	318	6.8e-33	-0.40	0.28		CYTOCHROME P450 ERYF; 1OXA_5 CHAIN: NULL 1OXA_6	OXIDOREDUCTASE (OXYGENASE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOLE	Compound	PDB annotation
1227	1crz	A	130	352	0.00032	-0.06	0.04	TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD	
1227	1ejj	A	116	431	4.8e-73	0.57	1.00	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER	
1227	1ejj	A	4	285	1.3e-58	0.40	0.29	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER	
1227	1ejj	A	65	373	1.6e-66	0.38	1.00	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER	
1227	1got	B	12	370	1.3e-77			119,11 GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMAL, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROOTRIMER 2 SIGNAL TRANSDUCTION	
1227	1got	B	14	328	1.3e-77	0.14	0.53	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMAL, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROOTRIMER 2 SIGNAL TRANSDUCTION	
1227	1got	B	166	431	4.8e-54	0.64	1.00	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMAL, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOLE	Compound	PDB annotation
										BINDING/TRANSDUCER), G PROTEIN, HETERO TRIMER 2 SIGNAL TRANSDUCTION
1235	1af	H	413	518	0.0068	-0.14	0.35	ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN C REGION, V REGION	
1235	1qun	B	321	580	1.2e-15	-0.00	-0.18	PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN	
1235	1qun	B	408	701	6.8e-16	0.11	-0.19	PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN	
1236	1fs2	A	214	293	0.00034	-0.25	0.13	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE	
1236	1pjr							PCRA; CHAIN: NULL;	HELICASE DNA REPAIR, DNA REPLICATION, SOS RESPONSE, HELICASE, 2 ATP-BINDING, DNA-BINDING	
1236	1uuu	A	441	872	3.2e-68	-0.22	0.58		ATP-DEPENDENT DNA HELICASE REP, CHAIN: A, B; DNA CHAIN: C;	COMPLEX (HELICASE/DNA)
1236	2pjr	A	436	991	1.3e-62			90.62	HELICASE PCRA; CHAIN: A, F;	COMPLEX (HELICASE/DNA), HELICASE, DNA UNWINDING HYDROLASE/DNA ATP-DEPENDENT

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	PMF score	SEQFOLD D score	Compound	PDB annotation
								HELICASE PCRA; CHAIN: B; G; DNA (5'-D(*TP*TP*TP*TP*T-3'); CHAIN: C, D; DNA (5'-D(*GP*C)-3'); CHAIN: H; DNA (5'-D(*AP*CP*TP*GP*C)-3'); CHAIN: I;	HELICASE PCRA; ATP-DEPENDENT HELICASE PCRA; HELICASE PCRA, HYDROLASE, DNA, PRODUCT COMPLEX
1237	1e4y	A	10	213	3.4e-22	-0.01	0.89	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE); COMPLEX (INHIBITOR/NUCLEASE); COMPLEX (R1-ANG), HYDROLASE 2, MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1237	1a4y	A	126	299	6.4e-07	0.04	0.09	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE); COMPLEX (INHIBITOR/NUCLEASE); COMPLEX (R1-ANG), HYDROLASE 2, MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1237	1a9n	A	12	151	3.4e-13	0.04	0.35	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1237	1a9n	A	20	101	3.2e-07	0.28	0.51	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1237	1a9n	A	51	187	8.5e-24	0.36	0.71	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1237	1a9n	A	72	196	3.4e-20	0.04	0.04	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1237	1a9n	C	20	101	3.2e-07	0.49	0.35		U2 RNA HAIRPIN IV; CHAIN: Q; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	SNRNP, RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1237	1a9n	C	51	192	5.1e-24	0.05	0.66		U2 RNA HAIRPIN IV; CHAIN: Q; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1237	1d0b	A	3	187	3.2e-25	-0.14	0.71		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1237	1d0b	A	44	221	6.8e-29	-0.20	0.07		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1237	1d0b	A	75	268	6.4e-21	0.15	-0.02		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1237	1dce	A	11	100	1.6e-11	0.35	0.96	RAB	GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYL METHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1dce	A	130	233	3.2e-13	0.47	0.94	RAB	GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYL METHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1dce	A	160	278	4.8e-10	0.20	-0.03	RAB	GERANYLGERANYLTRANSFERASE	TRANSFERASE CRYSTAL STRUCTURE, RAB

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLE D score	Compound	PDB annotation
									RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE; FORMYLMEITHIONINE, ALPHA SUBUNIT, BETA SUBUNIT B,D;	GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMEITHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1dce	A	44	169	3.2e-11	0.21	0.33	RAB	GERANYLGERANYLTRANSFERASE; RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE; FORMYLMEITHIONINE, ALPHA SUBUNIT, BETA SUBUNIT B,D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMEITHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1ds9	A	11	146	4.8e-12	-0.31	0.09			
1237	1ds9	A	130	252	3.2e-14	-0.20	0.22		OUTER ARM DYNEN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEN, 2 CHLAMYDOMONAS, FLAGELLA
1237	1ds9	A	37	169	1.6e-11	-0.54	0.45		OUTER ARM DYNEN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEN, 2 CHLAMYDOMONAS, FLAGELLA
1237	1f61	A	132	192	1.1e-06	-0.03	0.65		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1237	1f61	B	132	192	1.1e-06	0.25	0.60		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1237	1fs2	A	10	206	1.2e-25	0.15	0.46		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2-

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1237	1fs2	A	I30	294	1.1e-06	0.34	0.22		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1237	2bnh		19	223	1.5e-28	-0.03	0.82		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOTENSIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1238	1a17		119	279	1e-18	0.10	0.80		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		133	250	6.4e-14	0.27	0.51		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		153	296	4.8e-13	0.30	0.76		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		20	153	8e-13	0.01	0.23		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1238	1a17		221	368	5.1e-19	0.31	0.99		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		232	348	9.6e-13	0.56	0.94		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		263	392	9.6e-13	0.22	0.80		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		290	416	3.2e-14	0.22	0.52		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		29	142	1.7e-15	0.18	0.11		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		300	414	1.7e-18	-0.14	0.74		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		338	421	4.8e-13	0.41	0.37		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
		*								TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		56	184	1.7e-15	0.18	0.70	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;		STRUCTURE
1238	1a17		63	175	8e-10	0.34	0.41	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;		HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		85	209	4.8e-11	0.12	0.58	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;		STRUCTURE
1238	1a17		89	212	3.4e-17	0.12	0.65	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;		HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1d8d	A	217	410	4.8e-07	-0.23	0.60	FARNESYLTRANSFERASE (ALPHA SUBUNIT); CHAIN: A; FARNESYLTRANSFERASE (BETA SUBUNIT); CHAIN: B; K-RAS4B PEPTIDE SUBSTRATE; CHAIN: P;		STRUCTURE
1238	1d8d	A	28	266	3.4e-15	-0.04	0.18	FARNESYLTRANSFERASE (ALPHA SUBUNIT); CHAIN: A; FARNESYLTRANSFERASE (BETA SUBUNIT); CHAIN: B; K-RAS4B PEPTIDE SUBSTRATE; CHAIN: P;		TRANSFERASE FTASE; FTASE; FTASE, PFT, PFTASE, FARNESYLTRANSFERASE, FARNESYL 2 TRANSFERASE, CAAX, RAS, CANCER

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1238	1e96	B	135	278	1.4e-09	0.15	0.48		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	189	322	8e-10	0.40	0.76		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	229	379	4.8e-09	0.14	0.98		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	290	417	4.8e-09	0.05	0.86		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	62	244	0.00016	0.12	0.21		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1elr	A	133	247	6.4e-15	0.38	0.47		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	161	252	6.4e-15	0.24	1.00		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	195	283	1.6e-10	0.02	0.96		TPR2A-DOMAIN OF HOP;	CHAPERONE HOP, TPR-DOMAIN,

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQRFOL D score	Compound	PDB annotation
1238	1elr	A	228	326	4.8e-12	0.47	0.99		CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	262	355	3.2e-13	0.27	0.74		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	28	117	4.8e-11	0.13	0.29		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	334	419	4.8e-12	0.54	0.55		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	93	185	1.1e-11	0.31	0.33		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elw	A	135	221	1.1e-13	0.46	0.99		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	153	262	1.3e-12	0.47	0.96		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	196	296	3.2e-10	0.63	1.00		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	SEQFOL D score	Compound	PDB annotation
1238	1elw	A	236	332	4.8e-13	0.76	1.00	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	25	122	4.8e-10	0.32	0.57	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	2	99	6.4e-14	0.25	0.03	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	304	408	3.2e-15	0.23	0.98	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	342	419	1.1e-11	0.29	0.21	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	61	155	6.4e-10	0.32	0.82	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1fch	A	166	413	9.6e-38	0.32	1.00	PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRA TRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1fch	A	313	420	3.2e-09	0.07	0.96	PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
1238	1fch	A	34	273	6.4e-31	0.48	1.00		PEPTIDE; CHAIN: C, D;	PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1fch	A	7	220	1.3e-29	0.38	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1fch	A	98	345	4.8e-29	0.46	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1241	1edh	A	34	152	3.2e-20	0.10	0.55		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD2; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1241	1edh	A	52	253	6.8e-27	-0.19	0.76		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD2; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1241	1edh	A	83	255	4.8e-17	0.21	0.64		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1241	Inci	B	206	253	5.1e-06	-0.07	0.04		N-CADHERIN; INCL 3	AND 2, ECAD12, CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1241	Inci	B	56	152	1.7e-05	0.15	0.31		N-CADHERIN; INCL 3	CELL ADHESION PROTEIN
1241	Incj	A	34	152	1.4e-21	-0.20	0.28		N-CADHERIN; CHAIN: A;	CADHERIN INCL 13
1241	Incj	A	43	253	1.7e-21	-0.03	0.65		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN
1241	Incj	A	90	255	6.4e-17	-0.20	0.35		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
1241	Iqu0	A	358	549	3.4e-20	-0.08	0.40	LAMININ ALPHA2 CHAIN; CHAIN: A, B, C, D;	CELL ADHESION PROTEIN	CELL ADHESION PROTEIN
1241	1suh		43	154	1.7e-07	-0.22	0.04	EPITHELIAL CADHERIN; CHAIN: NULL;	METAL BINDING PROTEIN BETA SANDWICH, CALCIUM-BINDING PROTEIN, METAL BINDING 2 PROTEIN	METAL BINDING PROTEIN BETA SANDWICH, CALCIUM-BINDING PROTEIN, METAL BINDING 2 PROTEIN
1246	1a5e		132	262	3.4e-30	0.56	1.00	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		166	330	3.4e-30	0.40	1.00	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;		ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		202	359	5.1e-29	0.84	1.00	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;		ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		233	385	1.5e-29	0.39	0.93	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;		ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		233	393	3.4e-30		66.97	TUMOR SUPPRESSOR		ANTI-ONCOGENE CELL CYCLE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1246	lawc	B	145	298	1e-43	1.05		P16NK4A; CHAIN: NULL;	ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	lawc	B	14	165	1e-39	0.93	1.00	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION(DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION(DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawc	B	150	298	9.6e-41	0.97	1.00	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION(DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION(DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawc	B	17	165	1.6e-38	0.93	1.00	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION(DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION(DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsiBlast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1246	lawc	B	183	332	3.4e-39	0.84	1.00	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	
1246	lawc	B	184	332	9.6e-35	0.55	1.00	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	
1246	lawc	B	212	362	1e-40	0.77	1.00	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	
1246	lawc	B	212	363	1e-43		90.97	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	
1246	lawc	B	217	395	3.2e-32	0.21	0.23	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA;	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLE score	Compound	PDB annotation
									PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	3	132	1.6e-33	0.88	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	45	199	8.5e-39	0.55	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	50	199	9.6e-37	0.68	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1bd8								P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1246	1bd8								P19INK4D CDK4/6 INHIBITOR;	TUMOR SUPPRESSOR TUMOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR END AA	Psi Blast score	PMF D score	SEQFOL	Compound	PDB annotation
1246	1b17	B	244	365	1.7e-28	0.57	1.00	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;
1246	1b1x	B	114	304	3.4e-38	0.10	0.10	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
1246	1b1x	B	13	170	1.7e-39	0.93	1.00	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
1246	1b1x	B	147	303	6.8e-40		78.94	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
1246	1b1x	B	183	338	3.4e-38	0.73	1.00	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMIF score	SEQTOL D score	Compound	PDB annotation
1246	1blx	B	215	368	1.7e-38	0.89	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	(INHIBITOR PROTEINKINASE)
1246	1blx	B	50	205	1.5e-38	0.70	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	(INHIBITOR PROTEINKINASE)
1246	1blx	B	82	237	6.8e-40	1.03	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	(INHIBITOR PROTEINKINASE)
1246	1bu9	A	144	310	6.8e-37	0.78	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	(INHIBITOR PROTEINKINASE)
1246	1bu9	A	150	303	1.6e-36	0.97	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	(INHIBITOR PROTEINKINASE)
1246	1bu9	A	17	170	9.6e-37	0.87	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	(INHIBITOR PROTEINKINASE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1246	1bu9	A	181	338	1e-35	0.61	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	184	367	8e-33	0.25	0.99		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	215	373	3.4e-35	0.63	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	243	394	6.8e-33	0.79	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	3	174	3.4e-37	0.47	0.51		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	44	205	1.7e-39	0.94	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	9	177	1.7e-39			89.81	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQ/FOL D score	Compound	PDB annotation
1246	1ihb	A	150	302	6.4e-36	0.88	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	HORMONE/GROWTH FACTOR
1246	1ihb	A	17	169	3.2e-36	0.78	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	1ihb	A	184	366	3.2e-32	0.28	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	1ihb	A	81	236	3.2e-36				CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	1ikn	D	12	186	4.8e-35	0.47	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNFKB COMPLEX
1246	1ikn	D	179	346	1.6e-30	0.20	0.92		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNFKB COMPLEX
1246	1ikn	D	212	404	1.6e-34	0.22	0.35		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNFKB COMPLEX
1246	1ikn	D	45	232	8e-43	0.18	1.00		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOLE score	Compound	PDB annotation
1246	likn	D	45	253	8e-43				CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	lmyo	12	130	9.6e-25			80.97		CHAIN: A; NF-KAPPA-B P65 SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	lnfi	E	113	311	1.7e-48	0.69	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT COMPLEX (TRANSCRIPTION REGIANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	lnfi	E	11	186	1.4e-35	0.81	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGIANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT)
1246	lnfi	E	143	338	5.1e-47	0.55	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGIANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	lnfi	E	177	367	1.7e-48	0.62	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGIANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	lnfi	E	178	346	4.8e-30	0.65	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGIANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	PMIF score	SEQFOL D score	Compound	PDB annotation
1246	1nf1	E	17	170	3.4e-38	0.85	1.00	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1nf1	E	210	404	9.6e-35	0.26	0.21	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1nf1	E	215	394	1.5e-44	0.53	1.00	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1nf1	E	43	238	1.7e-51	0.53	1.00	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1nf1	E	43	242	1.7e-51		89.07	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1nf1	E	44	232	1.6e-42	0.74	1.00	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1nf1	E	82	278	5.1e-50	0.66	1.00	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT),

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1246	1sw6	A	76	320	1.3e-21		60.99	REGULATORY PROTEIN SWI6; CHAIN: A, B;		ANKYRIN 2 REPEAT HELIX TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1246	1ycs	B	214	398	3.2e-18		69.71	P53; CHAIN: A; 53BP2; CHAIN: B;		P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1250	1cun	A	375	591	5.1e-12	-0.03	0.29	ALPHA SPECTRIN; CHAIN: A, B, C;		STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1250	1cun	A	436	651	5.1e-07	0.02	0.03	ALPHA SPECTRIN; CHAIN: A, B, C;		STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1250	1hae		120	150	0.0051	0.07	0.11	HEREGULIN-ALPHA; CHAIN: NULL,		GROWTH FACTOR NEU DIFFERENTIATION FACTOR (RAT), ACETYLCHOLINE GROWTH FACTOR
1250	1hre		120	150	0.0051	0.13	0.25			GROWTH FACTOR HEREGULIN-ALPHA (EPIDERMAL GROWTH FACTOR-LIKE DOMAIN) 1HRE 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1HRE 4

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1252	1d4v	A	326	426	5.1e-10	0.10	-0.14		TNF RELATED APOPTOSIS INDUCING LIGAND; CHAIN: B; DEATH RECEPTOR 5; CHAIN: A;	APOPTOSIS TRAIL; DR5; LIGAND-RECEPTOR COMPLEX, TRIMERIC JELLY-ROLL; TNFR-2 SUPERFAMILY, APOPTOSIS
1252	1dan	L	351	449	8e-09	0.06	-0.13		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1252	1dx5	I	233	346	3.2e-12	0.02	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE, COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTI COAGULANT COMPLEX, 2 ANTI FIBRINOLYTIC COMPLEX
1252	1dx5	I	268	394	6.4e-15	0.03	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE, COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTI COAGULANT COMPLEX, 2 ANTI FIBRINOLYTIC COMPLEX
1252	1dx5	I	308	436	1.1e-12	0.10	-0.19		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE, COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTI COAGULANT COMPLEX, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PIRF score	SEQFOL D score	Compound	PDB annotation
1252	1emn			307	395	1.6e-13	0.24	0.04	FIBRILLIN; CHAIN: NULL;	ANTIFIBRINOLYTIC COMPLEX MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN MATRIX PROTEIN
1252	1emn								FIBRILLIN; CHAIN: NULL;	EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1252	1klo	L		225	419	8.5e-39	0.17	0.93	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN
1252	1klo			234	411	8.5e-39			LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1klo			293	452	1.6e-20	0.40	0.51	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1klo			358	496	3.2e-18	-0.00	-0.03	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1pkf	L		351	441	3.2e-09	0.10	-0.17	FACTOR IXA; CHAIN: C; L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1252	1skz			319	414	3.4e-17	0.34	-0.14	ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQROL D score	Compound	PDB annotation
1252	1skz		355	425	5.1e-10	0.16	0.19		ANTISTASIN; CHAIN: NULL;	INHIBITOR, THROMBOSIS SERINE PROTEASE INHIBITOR, FACTOR XA INHIBITOR, ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1252	1xka	L	355	448	3.2e-09	0.14	-0.18		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL GROWTHFACTOR LIKE DOMAIN
1252	4mt2		368	428	1.3e-09	-0.05	0.00		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	
1252	9wga	A	298	492	4.8e-15	0.04	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1253	1one	A	11	134	9.6e-61	0.25	1.00		ENOLASE; CHAIN: A, B; ENOLASE; 1PDZ 4 CHAIN: NULL; 1PDZ 5	LYASE 2-PHOSPHO-D-GLYCERATE HYDROLASE; LYASE, GLYCOLYSIS LYASE (CARBON-OXYGEN) 2-PHOSPHO-D-GLYCERATE DEHYDRATASE; 1PDZ 6
1253	1pdz		11	137	8e-63	0.15	1.00			
1256	1kpf		53	163	9.6e-41	0.96	1.00		PROTEIN KINASE C INTERACTING PROTEIN; CHAIN: NULL;	PROTEIN KINASE INHIBITOR PKC-I, PROTEIN KINASE C INHIBITOR 1, HINT PROTEIN KINASE INHIBITOR, PKC-I, HIT PROTEIN FAMILY, 2 HISTIDINE TRIAD PROTEIN FAMILY, NUCLEOTIDYL HYDROLASE, 3 NUCLEOTIDYL TRANSFERASE
1256	1lqf		53	163	9.6e-41		144.01		PROTEIN KINASE C	PROTEIN KINASE INHIBITOR PKC-I

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
									INTERACTING PROTEIN; CHAIN: NULL;	1. PROTEIN KINASE C INHIBITOR 1, HINT PROTEIN KINASE INHIBITOR, PKCL-1, HIT PROTEIN FAMILY, 2 HISTIDINE TRIAD PROTEIN FAMILY, NUCLEOTIDYL HYDROLASE, 3 NUCLEOTIDYL TRANSFERASE
1256	4rhn	47	163	6.4e-41					HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN; CHAIN: NULL;	NUCLEOTIDE-BINDING PROTEIN HINT; NUCLEOTIDE-BINDING PROTEIN
1256	4rhn	52	163	6.4e-41	0.86	1.00			HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN; CHAIN: NULL;	NUCLEOTIDE-BINDING PROTEIN HINT; NUCLEOTIDE-BINDING PROTEIN
1257	1a5e	39	151	1.4e-21	0.27	0.48			TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1a5e	39	154	8e-26	0.80	1.00			TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1a5e	61	162	3.4e-25	0.65	1.00			TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1a5e	6	121	4.8e-18	0.16	0.40			TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1awc	B	39	164	6.4e-37	0.61	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA 1; COMPLEX (TRANSCRIPTION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1257	1awc	B	4	154	9.6e-40	0.40	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1257	1bd8									
1257	1bi7	B	7	157	1.3e-31	0.48	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR CDK4/6 INHIBITOR, ANKYRIN MOTIF
1257	1bi7	B	39	154	3.2e-26	0.62	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1257	1bi7	B	6	121	8e-19	0.22	0.35		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1257	1bix	B	39	164	1.7e-32	0.82	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEINKINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOOL D score	Compound	PDB annotation
1257	1blx	B	7	157	1.6e-30	0.38	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	(INHIBITOR PROTEIN/KINASE)
1257	1bu9	A	6	159	8e-37	0.34	0.88		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1257	1d9s	A	39	154	1.6e-26	0.70	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1257	1d9s	A	6	127	3.2e-20	0.42	0.95		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1257	1dcq	A	2	91	6.4e-15	0.41	0.80		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1257	1dcq	A	71	157	1.1e-17	0.05	0.99		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1257	1ihb	A	6	158	4.8e-36	0.52	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A; B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1257	1ihb	A	73	163	8e-18	0.47	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A; B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1257	1ikn	D	4	162	8e-38	0.08	0.84		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1257	1myo		35	152	3.2e-26			52.27	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1257	1myo		40	156	3.2e-26	0.32	0.98		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1257	1myo		5	106	6.4e-24	0.22	0.98		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1257	1myo		74	164	1.1e-23	0.04	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1257	1nf1	E	4	162	1.6e-38	0.39	1.00		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B; D; I-KAPPA-B-ALPHA; CHAIN: E; F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRN 2 REPEAT HELIX
1257	1ycs	B	12	95	1.4e-19	0.04	0.86		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRN REPEATS) P53BP2; ANK YRN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, ³ POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANK YRN REPEATS)
1257	1ycs	B	39	154	1.6e-25	0.24	1.00		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRN REPEATS) P53BP2; ANK YRN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, ³ POLYMORPHISM, COMPLEX (ANTI-

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFFOL D score	Compound	PDB annotation
1257	1ycs	B	73	161	1.6e-22	0.44	1.00	P53; CHAIN: A; 53BP2; CHAIN: B;	ONCOGENE/ANKYRIN REPEATS COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1258	1afb	1	3	183	3.4e-20		52.08	MANNOSE-BINDING PROTEIN-A; 1AFB 4 CHAIN: 1, 2, 3; 1AFB 5	LECTIN CL-QPDWG; 1AFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1AFB 22
1258	1bj3	A	31	180	8e-34	0.42	0.11	COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERO DIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPER FAMILY, COLLAGEN BINDING PROTEIN
1258	1bj3	A	34	181	8e-34		61.48	COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERO DIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPER FAMILY, COLLAGEN BINDING PROTEIN
1258	1c3a	A	31	185	6.4e-28	0.20	0.89	FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
1258	1c3a	B	31	183	1.4e-30	0.03	0.01	FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOOL D score	Compound	PDB annotation
1258 1dv8	A	31	180	6.4e-28	0.72	0.68			ASIALOGLYCOPROTEIN RECEPTOR 1; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN H1; C-TYPE LECTIN CRD
1258 1e5u	I	52	80	0.0093	-0.69	0.57			INTIMIN; CHAIN: I;	INTIMIN INT190; INTIMIN, ESCHERICHIA COLI, CELL ADHESION, OUTER MEMBRANE 2 PROTEIN, NMR SPECTROSCOPY
1258 1egg	B	29	187	1.6e-29	0.41	0.36			MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR
1258 1esi		44	213	4.8e-30	0.45	0.89			CELL ADHESION PROTEIN E-SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1 - 157) IESL 3 (FORMERLY KNOWN AS ELAM-1) IESL 4	
1258 1f00	I	52	80	0.0093	-0.19	0.40	60.26		CELL ADHESION PROTEIN E-SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1 - 157) IESL 3 (FORMERLY KNOWN AS ELAM-1) IESL 4	
1258 1htm		12	184	1.3e-23			68.61		INTIMIN; CHAIN: I;	CELL ADHESION IMMUNOGLOBULIN-LIKE FOLD, C-TYPE LECTIN-LIKE FOLD
1258 1hup		8	183	6.4e-21			50.48		TETRANECTIN; CHAIN: NULL;	LECTIN TETRANECTIN, PLASMINOGEN BINDING, KRINGLE 4, ALPHA-HELICAL 2 COILED COIL, C-TYPE LECTIN, CARBOHYDRATE RECOGNITION DOMAIN
1258 1ixx	A	31	180	4.8e-32	0.21	0.21			1HUP 4 CHAIN: NULL; 1HUP 5 COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR;	C-OXIDATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD
1258 1ixx	A	34	181	4.8e-32			58.55		COAGULATION FACTORS	MOTIF, LOOP EXCHANGED DIMER COAGULATION FACTOR BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	PMF score	SEQFOL D score	Compound	PDB annotation
		*							IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1lxz	B	31	183	1.3e-29	0.24	0.45	IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;
1258	1ixx	B	34	183	1.3e-29			COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1lit		31	182	1.6e-31	0.51	0.30	LITHOSTATHINE; CHAIN: NULL	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;
1258	1lit		31	183	1.6e-31			LITHOSTATHINE; CHAIN: NULL	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1qdd	A	18	183	1.6e-31			LITHOSTATHINE; CHAIN: A; LECTIN	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN
1258	1qdd	A	31	182	1.6e-31	0.65	0.52	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1258	1rmn	1	3	183	5.1e-19			LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) IRTM 3.1 RTM 96	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1258	1tm3		28	184	1.2e-24			TETRANECTIN; CHAIN: NULL;	LECTIN TETRANECTIN, PLASMINOGEN BINDING, KRINGLE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
										4, C-TYPE LECTIN, 2 CARBOHYDRATE RECOGNITION DOMAIN
1258	2afp	A	29	179	1.6e-27	-0.06	0.54		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C-2 TYPE LECTIN, ANTIFREEZE PROTEIN
1259	1dap	A	1	33	4.8e-05	-0.51	0.13		DIAMINOPIMELIC ACID DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE DAPDH; NADP, DEHYDROGENASE, D-AMINO ACID DEHYDROGENASE, LYSINE 2 BIOSYNTHESIS, ASYMMETRIC DIMER, OXIDOREDUCTASE
1259	3gpd	R	2	336	0				491.59	OXIDOREDUCTASE (NAD\$(A)-ALDEHYDE(D)) D-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (E.C.1.2.1.12) 3GPD 4
1259	3gpd	R	3	336	0	0.93	1.00		OXIDOREDUCTASE (NAD\$(A)-ALDEHYDE(D)) D-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (E.C.1.2.1.12) 3GPD 4	
1263	1a7c	A	82	463	4.8e-91			115.78	PLASMINOGEN ACTIVATOR INHIBITOR TYPE I; CHAIN: A; PENTAPEPTIDE; CHAIN: B, C	COMPLEX (PROTEASE INHIBITOR/PEPTIDE) PAI-1; SERINE PROTEASE INHIBITOR, PAI-1, CARBOHYDRATE, INHIBITOR 2 COMPLEX, PEPTIDE
1263	1as4	A	88	430	0	0.25	0.96		ANTICHYMOTRYPSIN; CHAIN: A, B;	SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQTOL D score	Compound	FDB annotation
1263	1as4	A	90	438	0			104.85	ANTICHYMO TRYPSIN A; B;	ANTICHYMO TRYPSIN; SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR, ANTICHYMO TRYPSIN
1263	1ath	B	101	464	1.3e-96			102.92	HUMAN ANTITHROMBIN-III ANTITHROMBIN III 1ATH 3	
1263	1ath	B	85	464	1.3e-96	0.23	1.00		HUMAN ANTITHROMBIN-III ANTITHROMBIN III 1ATH 3	
1263	1by7	A	86	463	0	0.63	1.00		PLASMINOGEN ACTIVATOR INHIBITOR-2; CHAIN: A;	PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING
1263	1by7	A	86	463	0			101.02	PLASMINOGEN ACTIVATOR INHIBITOR-2; CHAIN: A;	PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING
1263	1d5s	B	433	463	1.3e-09	-0.75	0.04		P1-ARG ANTITRYPsin; CHAIN: A; P1-ARG ANTITRYPsin; CHAIN: B;	HYDROLASE INHIBITOR SERPIN FOLD, RCL CLEAVAGE, A BETA SHEET POLYMERISATION
1263	1db2	A	83	463	3.2e-94				PLASMINOGEN ACTIVATOR INHIBITOR-1; CHAIN: A; B;	HYDROLASE INHIBITOR NATIVE SERPIN, HYDROLASE INHIBITOR
1263	1ezx	A	86	432	0	0.23	0.80		ALPHA-1-ANTITRYPsin; CHAIN: A; ALPHA-1-ANTITRYPsin; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1-ANTITRYSIN, 2 TRYPSIN
1263	1hle	A	85	426	3.2e-98	0.38	1.00		HYDROLASE INHIBITOR(SERINE PROTEINASE) HORSE LEUKOCYTE ELASTASE INHIBITOR (HLE) 1HLE 3	
1263	1hle	A	85	432	3.2e-98			84.90	HYDROLASE INHIBITOR(SERINE PROTEINASE) HORSE LEUKOCYTE ELASTASE INHIBITOR (HLE) 1HLE 3	
1263	1ova	A	80	463	0			126.84	SERPIN OVALBUMIN (EGG ALBUMIN) IOVA 3	
1263	1ova	A	87	463	0	0.62	1.00		SERPIN OVALBUMIN (EGG	

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1263	1qip	A	86	463	0	0.49	1.00	ALBUMIN 1OVA 3	SERINE PROTEASE INHIBITOR, ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE.
1263	1qip	A	88	466	0		146.76	ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR, ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
1263	1qmb	B	433	463	4.8e-09	-0.75	0.12	ALPHA-1-ANTITRYPSIN; CHAIN: A, B;	SERINE PROTEASE INHIBITOR, ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-PI; SERPIN, ANTITRYPsin, POLYMER, CLEAVED
1263	1qmn	A	88	464	0	0.44	1.00	ALPHA-1-ANTICHYMOTRYPSIN; CHAIN: A;	SERPIN AACT SERPIN, SERINE PROTEINASE INHIBITOR, PARTIAL LOOP 2 INSERTION, LOOP-SHEET POLYMERIZATION, EMPHYSEMA, DISEASE 3 MUTATION, ACUTE PHASE PROTEIN, CONFORMATIONAL DISEASE
1263	1sek		80	463	3.2e-85		102.05	SERPINK; CHAIN: NULL;	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, SERPIN, PROTEASE
1263	2ant	I	47	466	0		139.88	ANTITHROMBIN; CHAIN: I;	SERPIN SERPIN, HEPARIN, INHIBITOR
1263	2ant	I	49	464	0	0.48	1.00	ANTITHROMBIN; CHAIN: I, I;	SERPIN SERPIN, HEPARIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsiBlast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1263	2ant	L	59	466	0		125.53	ANTITHROMBIN; CHAIN: L; I;		INHIBITOR SERPIN SERPIN, HEPARIN, INHIBITOR
1263	2ant	L	81	464	0	0.63	1.00	ANTITHROMBIN; CHAIN: L; I;		SERPIN SERPIN, HEPARIN, INHIBITOR
1264	1ain	A	25	218	6.4e-92	0.93	1.00	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;		COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1264	1ain	A	25	219	1.2e-93			237.20	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1264	1ain	A	26	210	1.2e-93	1.19	1.00	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;		COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1264	1agd	A	25	218	3.2e-92	0.97	1.00	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;		HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1264	1agd	A	25	219	3.2e-92			239.77	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1264	1agd	A	26	210	8.5e-92	0.98	1.00	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE		HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I,

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFFOL D score	Compound	PDB annotation
1264	1duz	A	25	218	1.6e-88	1.03	1.00		(GGKKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX
1264	1efx	A	25	218	9.6e-91	1.13	1.00		HLA-A*0201; CHAIN: A; D; BETA-2' MICROGLOBULIN; CHAIN: B; E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C; F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD RECEPTOR/MHC COMPLEX
1264	1efx	A	26	210	8.5e-93	1.29	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2'-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D; E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1264	1hoc	A	25	218	1.6e-84			206.63	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2'-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D; E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1264	1hsa	A	25	218	3.2e-91	0.91	1.00		HISTOCOMPATIBILITY ANTIGEN MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING 1HOC 3 OF H-2D-B—B2- MICROGLOBULIN, AND A 9-RESIDUE PEPTIDE 1HOC 4.	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHSA-3 /HLA-B(ASTERISK)2705\$ IHSA-4
1264	1hsa	A	25	219	3.2e-91			231.27	HISTOCOMPATIBILITY	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
1264	1hsb	A	25	218	3.2e-89	1.15	1.00	ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1264	1hsb	A	25	219	3.2e-89			HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN A W68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1264	1mhe	A	26	219	4.8e-88		226.78	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN A W68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1264	1qdd	A *	26	218	6.4e-89	1.17	1.00	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q; LEADER PEPTIDE 3	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHCE, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE 3 CLASSICAL MHC, CLASS IB MHC
1264	1tmc	A	25	199	9.6e-81		257.75	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
								HISTOCOMPATIBILITY ANTIGEN HLA-A-W68 ITMC3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPPEYHRK) ITMC 4	
1265	Ialn	A	25	212	0	0.82	1.00	B*3501; CHAIN: A; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1265	Ialn	A	25	213	0		222.84	B*3501; CHAIN: A; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1265	lagd	A	25	212	0	0.93	1.00	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1265	lagd	A	25	213	0		242.14	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1265	lelx	A	25	212	4.8e-100	0.96	1.00	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D; E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1265	Ihss	A	25	212	1.6e-100	1.04	1.00		HISTOCOMPATIBILITY

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1265	1hsa	A	25	213	1.6e-100				ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHSA 3 /HLA-B(ASTERISK)2705S IHSA 4	
1265	1qqd	A	26	212	1.3e-98	0.83	1.00	212.48	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHSA 3 /HLA-B(ASTERISK)2705S IHSA 4	
1265	1tmc	A	25	199	3.2e-93	1.00	1.00		HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1265	1tmc	A	25	199	3.2e-93				HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPPEYHRK) 1TMC 4	
1266	1aln	A	22	210	4.8e-97	0.88	1.00		B*3501; CHAIN: A, B; PEPTIDE YPLRPMVY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOLE score	Compound	PDB annotation
										ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1266	1aln	A	22	210	4.8e-97				B*3501; CHAIN: A; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1266	1agd	A	22	210	1.1e-97	0.92	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1266	1agd	A	22	210	1.1e-97				B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1266	1duz	A	22	208	4.8e-95	0.88	1.00		HLA-A*0201; CHAIN: A; D; BETA-2 MICROGLOBULIN; CHAIN: B; E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C; F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1266	1efx	A	22	210	3.2e-96	1.08	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2; MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D; E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1266	1hsa	A	22	210	3.2e-96	0.89	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHSAA3 /HLA-	

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
1266	1hsa	A	22	210	3.2e-96		195.27	B(ASTERISK)2705\$ 1HSA_4	
1266	1hsb	A	22	208	4.8e-96	0.87	1.00	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA_3 /HLA-B(ASTERISK)2705\$ 1HSA_4	
1266	1hsb	A	22	210	4.8e-96		189.34	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB_3 ANTIGEN) 1HSB_4	
1266	1qqd	A	23	210	3.2e-94	0.89	1.00	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1266	1tmc	A	22	197	4.8e-90	0.98	1.00	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC_3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPYHRK) 1TMC_4	
1266	1tmc	A	22	197	4.8e-90		228.77	HISTOCOMPATIBILITY ANTIGEN TRUNCATED	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPYHRK) 1TMC 4	
1267	1ain	A	25	214	6.4e-100	1.01	1.00	B*3501; CHAIN: A; PEPTIDE VPLRPMTY; CHAIN: C;		COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1267	1ain	A	25	214	6.4e-100		206.29	B*3501; CHAIN: A; PEPTIDE VPLRPMTY; CHAIN: C;		COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1267	1agd	A	25	214	1.6e-100	0.95	1.00	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;		HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1267	1agd	A	25	214	1.6e-100		193.54	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;		HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1267	1duz	A	25	214	3.2e-97	0.96	1.00	HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;		IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1267	1efx	A	25	214	1.6e-98	0.91	1.00	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-		IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFFOL D score	Compound	PDB annotation
								MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D; E;	IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1267	lhsa	A	25	214	1.6e-99	1.02	1.00	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHSA_3 /HLA-B(ASTERISK)2705\$ IHSA_4	
1267	lhsa	A	25	214	1.6e-99		198.64	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHSA_3 /HLA-B(ASTERISK)2705\$ IHSA_4	
1267	lhsb	A	25	214	1.1e-98	0.98	1.00	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IIHSB 3 ANTIGEN) IHSB 4	
1267	lhsb	A	25	214	1.1e-98		190.28	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IIHSB 3 ANTIGEN) IHSB 4	
1267	1qqd	A	26	214	4.8e-97	0.95	1.00	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1267	1tmc	A	25	200	6.4e-91	0.91	1.00	HISTOCOMPATIBILITY	

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMW score	SEQTOL D score	Compound	PDB annotation
								ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TM C 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPYEYHRK) 1TM C 4	
1267	1tmc	A	25	200	6.4e-91		227.42	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TM C 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPYEYHRK) 1TM C 4	
1268	1aln	A	25	301	0	0.83	1.00	B*3501; CHAIN: A, B; PEPTIDE VPPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1268	1aln	A	25	301	0		381.69	B*3501; CHAIN: A, B; PEPTIDE VPPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1268	1agd	A	25	301	0	0.79	1.00	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1268	1agd	A	25	301	0		382.18	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
1268	1dn2	A	224	314	0.00034	-0.28	0.00		(GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX
1268	1duz	A	25	300	0	0.83	1.00		IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A; B; ENGINEERED PEPTIDE; CHAIN: E, F;	IMMUNE SYSTEM FC IGG PHAGE DISPLAY PEPTIDE
1268	1efx	A	25	303	0	0.83	1.00		HLA-A*0201; CHAIN: A; D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1268	1hsa	A	25	301	0	0.80	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1268	1hsa	A	25	301	0	0.80	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$1HSA 4	
1268	1hsb	A	25	295	0	0.82	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1268	1hsb	A	25	295	0		416.11	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1268	1igt	B	224	308	1.6e-05	0.26	0.71	IMMUNOGLOBULIN INTACT MAE231; CHAIN: A, B, C, D	IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1268	1mco	H	189	310	1.7e-05	0.09	0.23	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION 1MCO 3	
1268	1mco	H	220	314	6.8e-06	0.30	0.48	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION 1MCO 3	
1268	1qqd	A	26	299	0	0.63	1.00	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1269	1aln	A	25	285	0	0.88	1.00	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1269	1aln	A	25	288	0		279.39	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1269	1agd	A	25	285	0	0.87	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8; HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1269	1agd	A	25	288	0			278.31	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8; HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1269	1duz	A	25	285	0	0.93	1.00		HLA-A*0201; CHAIN: A; D; BETA-2 MICROGLOBULIN; CHAIN: B; E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C; F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1269	1efx	A	25	285	0	0.94	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D; E;	IMMUNE SYSTEM MHC HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1269	1hsa	A	25	285	0	0.93	1.00			HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA.3/HLA-B(ASTERISK)2705\$ 1HSA.4
1269	1hsa	A	25	288	0			284.65		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA.3/HLA-B(ASTERISK)2705\$ 1HSA.4
1269	1hsb	A	25	285	0	0.83	1.00			HISTOCOMPATIBILITY ANTIGEN CLASS I

SEQ ID NO:	PDB ID	CHAI NID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
								HISTOCOMPATIBILITY ANTIGEN A W68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1269	1hsb	A	25	288	0		302.23	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN A W68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1269	1mhe	A	26	285	0	0.70	1.00	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (YMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHCE, HLA-E, MHC CLASS HLA-E, HLA-E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA-2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1269	1mhe	A	26	288	0		253.44	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (YMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHCE, HLA-E, MHC CLASS HLA-E, HLA-E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA-2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1269	1qgd	A	26	285	0	0.86	1.00	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (Ig)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOLE D score	Compound	PDB annotation
1269	1tmc	A	25	200	8e-88	0.97	1.00	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPHEYHRK) 1TMC 4	
1269	1tmc	A	25	200	8e-88		257.46	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPHEYHRK) 1TMC 4	
1271	1aln	A	25	218	1.4e-94	0.95	1.00	B*3501; CHAIN: A; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1271	1aln	A	25	219	5.1e-96		239.16	B*3501; CHAIN: A; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1271	1aln	A	26	210	5.1e-96	1.03	1.00	B*3501; CHAIN: A; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1271	1agd	A	25	218	3.2e-95	1.03	1.00	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1271	1agd	A	25	219	3.2e-95			HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1271	1diz	A	25	218	3.2e-91	0.93	1.00	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1271	1efk	A	25	218	1.6e-93	0.95	1.00	HLA-A*0201; CHAIN: A; D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1271	1efx	A	26	210	1e-95	1.16	1.00	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2; MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1271	1hsa	A	25	218	4.8e-94	0.99	1.00	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2; MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1271	1hsa	A	25	219	4.8e-94				
							235.85	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I	

SEQ ID NO:	PDB ID	CHAJ N ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
		*							
1271	1hsb	A	25	218	4.8e-92	1.11	1.00	HISTOCOMPATIBILITY ANTIGEN IHSB 3 /HLA-B(ASERISK)270SS IHSB 4	
								HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68:1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1271	1hsb	A	25	219	4.8e-92		238.52	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68:1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
								HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	
1271	1mhe	A	26	218	1.6e-92	0.94	1.00		MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHCE, HLA-E, MHC CLASS HLA-E, HLA-E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA-2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
									MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHCE, HLA-E, MHC CLASS HLA-E, HLA-E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA-2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1271	1mhe	A	26	219	1.6e-92		218.16	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	
									IMMUNE SYSTEM
1271	1qqd	A	26	218	1.6e-92	0.95	1.00	HISTOCOMPATIBILITY	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
									LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN; A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1271	1tmc	A	25	199	1.4e-83		267.94		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1272	1aln	A	25	213	8e-91	0.92	1.00	B*3501; CHAIN: A; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	
1272	1aln	A	25	213	8e-91		150.68	B*3501; CHAIN: A; B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	
1272	1agd	A	25	213	3.2e-91	0.79	1.00	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	
1272	1agd	A	25	213	3.2e-91		152.02	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFFOL D score	Compound	PDB annotation
1272	1duz	A	25	213	6.4e-90	0.75	1.00	HLA-A*0201; CHAIN: A; D; BETA-2 MICROGLOBULIN; CHAIN: B; E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C; F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1272	1efx	A	25	213	6.4e-91	0.89	1.00	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D; E;	IMMUNE SYSTEM MHC HLA- CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1272	1hsa	A	25	213	1.6e-90	0.92	1.00	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHSA 3 /HLA-B(ASTERISK)270\$ IHSA 4	
1272	1hsa	A	25	213	1.6e-90		151.46	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHSA 3 /HLA-B(ASTERISK)270\$ IHSA 4	
1272	1hsb	A	25	213	3.2e-91	0.87	1.00	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN A W68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1272	1hsb	A	25	213	3.2e-91		178.43	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN A W68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOU D score	Compound	PDB annotation
1272	1mhe	A	26	213	4.8e-87	0.92	1.00		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA-E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA-2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1272	1mhe	A	26	213	4.8e-87			144.34	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA-E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA-2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1272	1qgd	A	26	213	8e-89	0.67	1.00		HISTOCOMPATIBILITY IMMUNE SYSTEM IMMUNOGLOBULIN (G)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM	
1272	1tmc	A	25	201	9.6e-87	0.83	1.00		HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A, BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A W68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPPEYHRK) 1TMC 4
1272	1tmc	A	25	205	9.6e-87			215.19		HISTOCOMPATIBILITY ANTIGEN TRUNCATED

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TM C 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TM C 4	
1273	1ain	A	25	205	6.4e-97	0.98	1.00	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	
1273	1ain	A	25	219	6.4e-97		221.84	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	
1273	1agd	A	25	205	3.2e-97	1.14	1.00	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	
1273	1agd	A	25	219	3.2e-97		223.96	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	
1273	1duz	A	25	205	1.1e-95	1.27	1.00	HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B; E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD	
1273	1efx	A	25	205	4.8e-97	1.17	1.00	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR,	

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1273	1hsa	A	25	205	1.6e-96	1.12	1.00		MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D; E;	IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1273	1hsa	A	25	219	1.6e-96				HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHSA 3 /HLA-B(ASTERISK)2705\$ IHSA 4	
1273	1hsb	A	25	205	1.6e-97	1.03	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHSA 3 /HLA-B(ASTERISK)2705\$ IHSA 4	
1273	1hsb	A	25	218	1.6e-97				HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1273	1qqd	A	26	205	1.1e-95	1.07	1.00		HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA-CW4 CHAIN: A: BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C,	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1273	1tmc	A	25	199	1.6e-93	1.25	1.00		HISTOCOMPATIBILITY	

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TM C3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TM C4	
1273	1tmc	A	25	199	1.6e-93		273.81		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TM C3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TM C4	
1274	1buo	A	1	126	1.6e-22	0.30	1.00		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN; TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1274	1buo	A	5	128	3.4e-28	0.41	0.99		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN; TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1274	1gof		291	458	1.1e-11	0.05	0.17		OXIDOREDUCTASE(OXYGEN- A)) GALACTOSE OXIDASE	

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOIL D score	Compound	PDB annotation
1274	1gof			383	495	1.6e-08	0.27	0.13	(E.C.1.1.3.9)(PH 4.5) (GOF 3 OXIDOREDUCTASE/OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) (GOF 3	
1275	1cum	A		170	385	6.8e-09			ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA, HELICAL LINKER REGION, 2.2 TANDEM 3-Helix COILED-COILS, STRUCTURAL PROTEIN CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1275	1quu	A		180	415	3.4e-12			HUMAN SKELETAL MUSCLE ALPHA-ACTinin 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL,
1275	1sig			130	416	5.1e-05			RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA 70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1276	1abr	B		413	552	1.4e-09	0.45	0.40	COMPLEX (GLYCOSIDASE/CARBOHYDRATE) ABRIN-A COMPLEXED WITH TWO SUGAR CHAINS 1ABR 3	
1276	1ce7	B		441	552	1.2e-15	0.16	0.21	RIBOSOME-INACTIVATING PROTEIN TYPE II; CHAIN: A; RIBOSOME-INACTIVATING PROTEIN TYPE II; CHAIN: B	RIBOSOME INACTIVATING PROTEIN TYPE II
1276	1ce7	B		450	543	0.00011	-0.25	0.13	RIBOSOME-INACTIVATING PROTEIN TYPE II; CHAIN: A; RIBOSOME-INACTIVATING PROTEIN TYPE II; CHAIN: B	RIBOSOME INACTIVATING PROTEIN TYPE II
1276	1qgq	A		123	345	6.4e-22	0.09	0.28	SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN	TRANSFERASE GLYCOSYLTRANSFERASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOIL D score	Compound	PDB annotation
1276	1xyf	A	44I	543	1.6e-16	-0.02	0.66		CHAIN: A; ENDO-1,4-BETA-XYLANASE; CHAIN: A, B;	HYDROLASE XYLAN DEGRADATION
1276	2aa1	B	44I	543	1.3e-07	-0.31	0.03		GLYCOSIDASE RICIN (E.C.3.2.2.22) 2AA1 3	
1279	2ak3	A	1	38	1.3e-16	-0.87	0.98		TRANSFERASE (PHOSPHOTRANSFERASE) ADENYLATE KINASE ISOENZYME-3 (GTP-AMP PHOSPHOTRANSFERASE) 2AK3 3 (E.C.2.7.4.10) 2AK3 4	
1280	12e8	H	59	253	1.3e-38	0.01	0.21		2E8 (IGG1=KAPPA=) ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN IMMUNOGLOBULIN
1280	1a0q	H	50	254	6.4e-37			61.67	29G11 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, ESTERASE
1280	1a0q	H	59	253	6.4e-37	-0.31	0.27		29G11 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, ESTERASE
1280	1a3r	H	50	256	1.3e-36		60.58	IGG2A; CHAIN: L, H; HUMAN RHINOVIRUS CAPSID PROTEIN VP2; CHAIN: P;	COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE) ANTIBODY 8F5; IMMUNOGLOBULIN, ANTIBODY, RHINOVIRUS, NEUTRALIZATION, 2 CONTINUOUS EPITOPE, COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE)	
1280	1a4j	L	51	252	9.6e-37	-0.11	0.17		IMMUNOGLOBULIN, DIELS ALDER CATALYTIC ANTIBODY; CHAIN: L, H, A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY, CATALYTIC ANTIBODY, DIELS ALDER, 2 GERMINE
1280	1a5f	H	48	256	3.2e-35		61.06	MONOCLONAL ANTI-E- SELECTIN 7A9 ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB, ANTIBODY, ANTI-E-SELECTIN	

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1280	1adq	L	50	255	1.1e-37	-0.04	0.00		IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;	IMMUNOGLOBULIN/AUTOANTIGEN COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
1280	1afv	H	52	253	4.8e-37	0.08	0.58		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
1280	1axt	H	51	256	4.8e-33			56.82	IMMUNOGLOBULIN IGG2A; CHAIN: L, H;	IMMUNOGLOBULIN, ANTIBODY FAB, CATALYST, ALDOLASE REACTION
1280	162w	L	51	258	8e-39	0.04	-0.07		ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRYCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
1280	1b4j	L	51	258	1.4e-37	0.00	0.09		ANTIBODY; CHAIN: L, H;	ANTIBODY ENGINEERING, ANTI BODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODIES, 2 FAB, X-RAY STRUCTURES, GAMMA-INTERFERON
1280	1b6d	A	51	252	4.8e-37	-0.12	0.13		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN, KAPPA LIGHT-

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1280 1bjf	L	51	252	8e-38	0.09	-0.09		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	CHAIN DIMER HEADER COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOTENSINIC FACTOR
1280 1bin	A	47	252	4.8e-35			57.09	MONOCLONAL ANTIBODY MRK-16 (LIGHT CHAIN); CHAIN: A, C; MONOCLONAL ANTIBODY MRK-16 (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNE SYSTEM
1280 1bm3	H	51	238	1.6e-34			57.73	IMMUNOGLOBULIN OPG2 FAB, CONSTANT DOMAIN; CHAIN: L; IMMUNOGLOBULIN OPG2 FAB, VARIABLE DOMAIN; CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN
1280 1bqj	H	50	255	3.2e-36			59.53	COMPLEX (ANTIBODY/ANTIGEN) HYHEL-5 FAB COMPLEXED WITH BOB WHITE QUAIL LYSOZYME IBQL 3.1BQL 95	
1280 1bz7	B	51	250	1.6e-26			57.49	ANTIBODY R24 (LIGHT CHAIN); CHAIN: A; ANTIBODY R24 (HEAVY CHAIN); CHAIN: B;	IMMUNE SYSTEM ANTIBODY (FAB FRAGMENT), IMMUNE SYSTEM
1280 1cel	L	51	232	9.6e-37	0.11	-0.03		CAMPATH-1H: LIGHT CHAIN; CHAIN: L; CAMPATH-1H: HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
1280 1cr9	H	59	255	8e-39	-0.12	0.60		FAB ANTIBODY LIGHT CHAIN; CHAIN: L; FAB ANTIBODY HEAVY CHAIN; CHAIN: H;	IMMUNE SYSTEM ANTI-PRION FAB 3F4; ANTI-PRION FAB 3F4 ANTI-PRION ANTIBODY, FAB 3F4
1280 1fbj	H	48	255	1.6e-36			56.80	COMPLEX (ANTIBODY/ANTIGEN) FAB FRAGMENT OF THE	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLE D score	Compound	PDB annotation
									MONOCLONAL ANTIBODY F9.13.7 (IGG1) 1FB1 3 COMPLEXED WITH LYSOZYME (E.C.3.2.1.17) 1FB1 4	
1280	1fir	H	51	256	3.2e-33		56.39		4-4-20 (IG*G2A=KAPPA=) FAB FRAGMENT; 1FLR 5 CHAIN: L, H; 1FLR 6	IMMUNOGLOBULIN
1280	1fdv	A	51	258	1.4e-37	0.11	-0.12		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
1280	1fdv	B	51	258	6.4e-32		57.20		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
1280	1hyx	L	47	255	1.3e-34		57.33		IMMUNOGLOBULIN 6D9; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY 6D9 CATALYTIC ANTIBODY, ESTER HYDROLYSIS, ESTEROLYTIC, FAB, 2IMMUNOGLOBULIN
1280	1iai	H	48	254	4.8e-33		60.65		IDIOTYPIC FAB 730.1.4 (IGG1) OF VIRUS 1IA1 5 CHAIN: L, H; 1IA1 7 ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A); 1IA1 9 CHAIN: M, 1IA1 10	COMPLEX (IMMUNOGLOBULIN IGG1/IGG2A)
1280	1igc	H	51	258	1.6e-32		57.26		COMPLEX (ANTIBODY/BINDING PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) IIGC 5 PROTEIN G, STREPTOCOCCUS IIGC 15	
1280	1igf	L	47	258	8e-35		58.26		IMMUNOGLOBULIN IGG1 FAB FRAGMENT (B1312) IIGF 3	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1280	1igy	B	59	253	1.6e-36	0.02	0.37	IGG1 INTACT ANTIBODY MAB61.1;3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
1280	1kel	H	51	255	6.4e-34		57.31	28B4 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY SULFIDE OXIDATION, MONOOXYGENASE, OXYGENATION, FAB, ² IMMUNOGLOBULIN, CATALYTIC ANTIBODY
1280	1mlb	B	48	258	8e-36		56.48	IMMUNOGLOBULIN FAB D44.1	
1280	1nct		178	254	0.0015	0.08	0.35	(IGG1,KAPPA) (BALB/C MOUSE, MONOCLONAL ANTIBODY) 1MLB_5; TTRN; CHAIN: NULL;	NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN_2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1280	1ngp	H	51	253	6.4e-37	-0.09	0.22	N1G9 (IGG1-LAMBDA=); CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN,
1280	1sm3	H	51	256	1.6e-36		58.83	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)
1280	1sm3	H	59	253	1.6e-36	-0.09	0.41	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)
1280	1sm3	L	50	252	3.2e-30		56.66	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1280	1tet	H	48	256	6.4e-36			57.32	IMMUNOGLOBULIN IGG1 MONOCLONAL FAB FRAGMENT (TE33) COMPLEX WITH CHOLERA 1TET 3 TOXIN PEPTIDE 3 (C1P3) 1TET 4	2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)
1280	1nmn		178	254	0.0051	-0.05	0.05		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1280	1wej	H	59	253	3.2e-37	0.55	0.70		E8 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: F;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C, ANTIGEN; IMMUNOGLOBULIN, IGG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C, COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
1280	1wwc	A	164	254	0.0051	-0.18	0.01		NT-3 GROWTH FACTOR RECEPTOR TRKC; CHAIN: A;	TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D-DOMAIN SWAPPING, 2 TRANSFERASE
1280	25c8	H	48	254	1.1e-37			57.06	IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CLOSURE REACTION
1280	25c8	H	59	253	1.1e-37	0.11	0.53		IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CLOSURE REACTION
1280	2cgf	H	51	254	1.6e-31			57.12	IMMUNOGLOBULIN IGG2B (KAPPA) FAB FRAGMENT COMPLEXED WITH ANTIGEN 2CGR 3 N-(P-CYANOPHENYL)-N'-(DIPHENYLEMETHYL)	

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQTOL D score	Compound	PDB annotation
1280	2fgw	L	51	258	1.6e-38	0.00	-0.08		GUANIDINEACETIC ACID 2CGR 4	
1280	2hni	C	47	258	4.8e-33			56.78	IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'HS2' (FHUH52-OZ FAB) 2FGW 4	HIV-1 REVERSE TRANSCRIPTASE; CHAIN: A, B; MONOCLONAL ANTIBODY 28; CHAIN: C, D; DNA; CHAIN: E, F;
1280	7fab	H	49	255	3.2e-31			57.01	IMMUNOGLOBULIN FAB' NEW (LAMBDA LIGHT CHAIN) 7FAB 3	IMMUNOGLOBULIN (LAMBDA LIGHT CHAIN) 7FAB 3
1284	1ckk	A	1	46	3.2e-19	-0.83	0.27		CREATINE KINASE; CHAIN: A, B, C, D;	TRANSFERASE TRANSFERASE, CREATINE KINASE
1284	1qh4	A	1	46	4.8e-19	-0.83	0.30		CREATINE KINASE, B CHAIN; CHAIN: A, B, C, D;	TRANSFERASE BB-CK; BRAIN-TYPE CREATINE KINASE; BRAIN-TYPE CELLULAR ENERGY 2
1284	1qkl	A	1	46	6.4e-19	-0.83	0.33		CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL; CHAIN: A, B, C, D, E, F, G, H;	CREATINE KINASE (CREATINE KINASE) UMTCK, MTA-CK; MITOCHONDRIAL CREATINE KINASE, CANCER, CELLULAR ENERGY 2 METABOLISM, GUANIDINO KINASE, MITOCHONDRIAL PERMEABILITY 3 TRANSITION, OCTAMER STABILITY
1284	2ckk	A	1	46	1.4e-19	-0.83	0.19		CREATINE KINASE; CHAIN: A;	TRANSFERASE CREATINE KINASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1287	1bq0	5	69	1.1e-27	0.89	1.00			DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
1287	1bq0	5	78	1.1e-27			68.92		DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
1287	1hdj	10	77	3.4e-30	0.77	1.00			HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDI-1; MOLECULAR CHAPERONE
1287	1hdj	5	80	3.4e-30			83.03		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDI-1; MOLECULAR CHAPERONE
1287	1hdj	7	69	1.6e-27	1.26	1.00			HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDI-1; MOLECULAR CHAPERONE
1292	1pbw	A	112	300	6.4e-08		93.22		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHODIESTERASE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, SH3 SIGNAL TRANSDUCTION
1292	1pbw	B	112	314	8e-09		94.15		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHODIESTERASE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, SH3 SIGNAL TRANSDUCTION
1292	1rgp	99	288	4.8e-17			109.76		RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE-ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION COMPLEX(GTPASE ACTIVATOR/PROTO-ONCOGENE)
1292	1x4	A	105	302	1.1e-17		114.46		P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN	ACTIVATOR/PROTO-ONCOGENE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
								RHOA; CHAIN: B;	GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1293	1bqq	M	112	281	9.6e-54		103.34	MEMBRANE-TYPE MATRIX METALLOPROTEINASE; CHAIN: M; METALLOPROTEINASE INHIBITOR; CHAIN: T;	(METALLOPROTEINASE/RECEPTOR COMPLEX) CDMT1-MMP; TIMP-2/MATRIX METALLOPROTEINASE, TISSUE INHIBITOR OF 2, METALLOPROTEINASES, PROTEINASE COMPLEX, PRO-GELATINASE A, 3 ACTIVATOR, CRYSTAL STRUCTURE, COMPLEX 4 (METALLOPROTEINASE/RECEPTOR)
1293	1cge								
1293	1cge		110	254	8e-60		120.96	HYDROLASE (METALLOPROTEASE) COLLAGENASE (E.C.3.4.24.7) (CATALYTIC DOMAIN) CRYSTAL FORM 1 1CGE 3	
1293	1ciz	A	107	272	4.8e-63		132.96	STROMELYSIN-1; CHAIN: A;	METALLOPROTEINASE MATRIX METALLOPROTEINASE-3; MATRIX METALLOPROTEINASE, MMP-3, NON-PEPTIDE INHIBITOR
1293	1ck7	A	25	699	0		647.13	GELATINASE A; CHAIN: A;	HYDROLASE MMP-2,72D TYPE IV COLLAGENASE; HYDROLASE (METALLOPROTEASE), FULL-LENGTH, METALLOPROTEINASE, 2 GELATINASE A
1293	1cxw	A	274	333	9.6e-14		90.80	HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	HYDROLASE COL-2; BETA SHEET, ALPHA HELIX, HYDROLASE
1293	1fbl		107	449	3.2e-70		151.00	FIBROBLAST (INTERSTITIAL)	METALLOPROTEINASE

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsiBlast Verify score	PMF score	SEQFOIL D score	Compound	PDB entry
1293	1gen		474	699	9.6e-50		99.59	GELATINASE A; CHAIN: NULL;	HYDROLASE (MMP-1); 1FBL 4 CHAIN; NULL; 1FBL 5
1293	1hfc		115	265	8e-60		117.07	METALLOPROTEASE FIBROBLAST COLLAGENASE (E.C.3.4.24.7) 1HFC 3	METALLOPROTEASE MMP-9, PUMP-1, MATRIN; 1MMQ 7
1293	1mmq		107	279	8e-56		119.28	MATRILYSIN; IMMQ 5 CHAIN: NULL; IMMQ 6	METALLOPROTEASE MMP-9, PUMP-1, MATRIN; 1MMQ 7
1293	1pex		477	699	4.8e-63		84.70	COLLAGENASE-3; CHAIN: NULL;	METALLOPROTEASE MMP-13; C-TERMINAL HEMOPEXIN-LIKE DOMAIN OF MATRIX-METALLOPROTEINASE
1293	1qib	A	112	272	1.6e-57		144.06	GELATINASE A; CHAIN: A;	HYDROLASE MATRIX METALLOPROTEINASE-2; INHIBITOR, MATRIXIN, MATRIX METALLOPROTEINASE-2 (MMP-2), 2 GELATTINASE A, METZINCIN, HYDROLASE
1293	1stm		44	272	1.6e-82		187.06	STROMELYSIN-1; CHAIN: NULL;	HYDROLASE MATRIX METALLOPROTEINASE-3, PROTEOGLYCANASE; HYDROLASE, METALLOPROTEASE, FIBROBLAST, COLLAGEN DEGRADATION
1293	830c	A	107	267	1.6e-59		138.28	MMP-13; CHAIN: A, B;	MATRIX METALLOPROTEASE MMP-13; MATRIX METALLOPROTEASE
1294	1ck7	A	25	432	0		419.38	GELATINASE A; CHAIN: A;	HYDROLASE MMP-2,72KD TYPE IV COLLAGENASE; HYDROLASE (METALLOPROTEASE), FULL-

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/FOL D score	Compound	PDB annotation
1294	1cxw	A	274	333	3.2e-21			90.47	HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	LENGTH, METALLOPROTEINASE, 2 GELATINASE A.
1297	2uez		400	562	3.2e-44			80.92	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	HYDROLASE COL-2; BETA SHEET, ALPHA HELIX, HYDROLASE UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
1298	1bh	A	1462	1834	8e-44			176.45	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1298	1fnf		1660	2042	8e-18			104.50	FIBRONECTIN; IFNF 6 CHAIN; NULL; IFNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
1298	1itb	B	1370	1645	3.2e-18			104.57	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	IMMUNOGLOBULIN/RECEPTOR Q IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1301	1agr	E	45	172	4.8e-48			146.45	GUANINE NUCLEOTIDE-BINDING PROTEIN G(D); CHAIN: A, D; RGS4; CHAIN: E, H;	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR) G-ALPHA-1; REGULATOR OF G-PROTEIN SIGNALLING 4; G-ALPHA-1, HYDROLASE, SIGNAL TRANSDUCTION, RGS4, 2 COMPLEX (SIGNAL TRANSDUCTION/REGULATOR), GTP-BINDING, 3 GTPASE ACTIVATING PROTEIN
1301	1agr	H	54	169	6.4e-43			133.76	GUANINE NUCLEOTIDE-	COMPLEX (SIGNAL

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
								BINDING PROTEIN G(); CHAIN: A; D; RGS4; CHAIN: E; H;	TRANSDUCTION/REGULATOR) G-ALPHA-1; REGULATOR OF G-PROTEIN SIGNALLING 4; G-ALPHA-1, HYDROLASE, SIGNAL TRANSDUCTION, RGS4, 2 COMPLEX (SIGNAL TRANSDUCTION/REGULATOR), GTP-BINDING, 3 GTPase ACTIVATING PROTEIN
1301	1cmz	A	46	172	3.2e-46	121.40	GAP (G-ALPHA INTERACTING) PROTEIN; CHAIN: A;	SIGNALING PROTEIN REGULATION GALPHA INTERACTING PROTEIN; GAP, RGS, REGULATOR OF G PROTEIN, SIGNALING PROTEIN 2 REGULATION	
1302	1a4i	A	5	235	4.8e-74	94.97	METHYLENETETRAHYDROFOLATE DEHYDROGENASE / CHAIN: A, B;	OXIDOREDUCTASE METHYLENETHF DEHYDROGENASE / METHENYLTHF THF, BIFUNCTIONAL, DEHYDROGENASE, CYCLOHYDROLASE, FOLATE, 2 OXIDOREDUCTASE HEADER	
1302	1b0a	A	1	235	8e-77	106.54	FOLD BIFUNCTIONAL PROTEIN; CHAIN: A;	OXIDOREDUCTASE, HYDROLASE FOLATE, DEHYDROGENASE, CYCLCOHYDROLASE, BIFUNCTIONAL, 2 CHANNELING, OXIDOREDUCTASE, HYDROLASE	
1307	1awc	B	18	157	8e-34	-0.23	0.52	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING,

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOIL Compound	PDB annotation
1307	1awc	B	3	125	4.8e-29	-0.09	0.29	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA; 1; CHAIN: B; DNA; CHAIN: D; E;	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPBALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1307	1bd8								TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1307	1bi7	B	443	560	6.4e-17	0.14	0.04	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTIONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTIONCOGENE) HEADER
1307	1blk	B	21	160	6.4e-26	-0.17	0.00	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEINKINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEINKINASE)
1307	1blk	B	50	183	1.3e-23	0.01	0.37	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEINKINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	PMIF score	SEQTOL D score	Compound	PDB annotation
1307	1bu9	A	1	130	6.4e-25	-0.12	0.15	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	(INHIBITOR PROTEINKINASE)
1307	1d9s	A	443	567	1.6e-17	0.14	0.06	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	HORMONE/GROWTHFACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR SIGNALLING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1307	1ihb	A	18	161	1.3e-25	-0.12	0.10	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A; B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1307	1ihb	A	1	129	3.2e-24	0.01	0.37	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A; B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1307	1myo		19	127	1.6e-20	0.14	0.01	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1314	1by2		26	138	1.1e-44		112.99	MAC-2 BINDING PROTEIN; CHAIN: NULL;	EXTRACELLULAR MODULE TUMOR-ASSOCIATED ANTIGEN 90K; EXTRACELLULAR MODULE, SCAVENGER RECEPTOR, TUMOUR-ASSOCIATED 2 ANTIGEN, EXTRACELLULAR MATRIX, GLYCOSYLATED PROTEIN
1315	1ae1	A	34	304	1.6e-66		73.73	TROPINONE REDUCTASE-I; CHAIN: A; B;	OXIDOREDUCTASE OXIDOREDUCTASE, TROPOANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1315	lael	B	*	304	9.6e-63		76.92	TROPINONE REDUCTASE-I; CHAIN: A, B;	DEHYDROGENASE; OXIDOREDUCTASE; TROPANE ALKALOID BIOSYNTHESIS; REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE
1315	1b6b			35	314	1.6e-47	65.57	CIS-BIPHENYL-2,3-DIHYDRODIOL-2,3-DEHYDROGENASE; CHAIN: NULL;	OXIDOREDUCTASE NAD-DEPENDENT OXIDOREDUCTASE; SHORT-CHAIN ALCOHOL 2 DEHYDROGENASE; PCB DEGRADATION
1315	1cyd	A	35	297	3.2e-54		69.13	CARBONYL REDUCTASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE, OXIDOREDUCTASE
1315	1f6s			38	319	4.8e-32	79.80	17-BETA-HYDROXYSTEROID-DEHYDROGENASE; CHAIN: NULL;	DEHYDROGENASE, 17-BETA-HYDROXYSTEROID
1315	1fmnc	A	30	298	6.4e-66		82.26	7 ALPHA-HYDROXYSTEROID DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE/REDUCTASE, BILE ACID CATABOLISM
1315	1hdc	A	35	306	4.8e-67		74.82	OXIDOREDUCTASE 3-ALPHA, 20-BETA-HYDROXYSTEROID DEHYDROGENASE (E.C.1.1.1.53) 1HDC 3 COMPLEXED WITH CAREBENOXOLONE 1HDC 4	
1315	1oaa			35	297	3.2e-21	65.22	SEPIAPTERIN REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE SEPIAPTERIN REDUCTASE, TETRAHYDROBIOPTERIN, OXIDOREDUCTASE
1315	1ybv	A	24	308	3.2e-61		82.44	TRIHYDROXYPHTHALENE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE NAPHTHOL REDUCTASE, OXIDOREDUCTASE
1315	2ae2	A	32	291	9.6e-65		76.67	TROPINONE REDUCTASE-II;	OXIDOREDUCTASE

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	SEQFOL D score	Compound	PDB annotation
								CHAIN: A; B;	OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO PSEUDOTROPTINE, SHORT-CHAIN DEHYDROGENASE
1321	1pbk		224	339	1.3e-24		194.11	FKBP25; CHAIN: NULL;	ISOMERASE FKBP25 C-TERMINAL DOMAIN; FKBP12 HOMOLOGOUS DOMAIN OF HFKBP25, ISOMERASE
1323	1am4	D	31	218	3.2e-43		50.20	P50-RHOGAP; CHAIN: A, B, C; CDC42HS; CHAIN: D, E, F;	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING) COMPLEX (GTPASE-ACTIVATING/GTP-BINDING), GTPASE ACTIVATION
1323	1byu	A	29	244	3.2e-32		61.74	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT I, TRANSPORT PROTEIN
1323	1byu	B	27	245	4.8e-33		64.26	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT I, TRANSPORT PROTEIN
1323	1cly	A	31	203	4.8e-64		79.57	RAS RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONCOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALLING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1323	1otq	A	33	204	1.3e-64		93.92	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1323	1cxz	A	28	204	1.6e-50		52.92	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B;	SIGNALING PROTEIN PROTEIN-PROTEIN COMPLEX, ANTI-PARALLEL COILED-COIL
1323	1ibr	A	34	209	1.1e-31		60.48	RAN; CHAIN: A, C; IMPORTIN	SMALL GTPASE KARYOPHERIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMW score	SEQFOL D score	Compound	PDB annotation
1323	1kao	31	204	6.4e-61			91.54		BETA SUBUNIT; CHAIN: B, D;	BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1323	1mb1	30	222	1.6e-51			62.77		RAP2A; CHAIN: NULL;	GTP-BINDING PROTEIN GTP-BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS
1323	1tp	C	31	227	1.1e-31		59.75		RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
1323	1zbd	A	29	209	9.6e-58		63.61		RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
1323	2ngf	A	33	230	1.6e-46		57.05		RAB-3A; CHAIN: A;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, ABCCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1323	3rab	A	30	204	1.6e-58		67.16		RAB3A; CHAIN: A;	GTP BINDING PROTEIN (G25K); HYDROLASE CDC42/CDC42GAP; CDC42/CDCC42GAP, TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3., HYDROLASE
1324	1a6o		167	536	1.6e-80		107.93		PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	HYDROLASE VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
										TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1324	1aq1		196	503	0		129.21	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	SER/THR KINASE PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUBROSPORINE, 2, CELL DIVISION, MITOSIS, INHIBITION
1324	1bi8	A	197	493	1.6e-81		122.05	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE, CYCLIN-INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITOR 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1324	1blk	A	192	499	3.2e-91		133.50	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1324	1cmk	E	160	503	8e-48		102.25	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) 1CMK 4 TRANSFERASE (PHOSPHOTRANSFERASE) CAMP-	
1324	1cp	E	165	503	3.2e-47		102.19	DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3 (CATALYTIC SUBUNIT) 1CTP 4 HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	
1324	1hc1		196	503	0		141.09	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION	

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOOL D score	Compound	PDB annotation
1324	1ian		180	567	1.6e-97			117.40	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE,
1324	1jnk		180	563	9.6e-100			136.35	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE TRANSFERASE JNK3;
1324	1kob	A	170	522	1.6e-51			105.97	TWITCHIN; CHAIN: A, B;	TRANSFERASE, JNK3 MAP KINASE, KINASE TWITCHIN, INTRASTERIC REGULATION
1324	1p38		179	570	0			150.88	MAP KINASE P38; CHAIN: NULL;	ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1324	1pme		190	568	0			128.64	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1324	3erk		181	509	0			140.27	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1325	1a6o		167	496	6.4e-80			108.11	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE CK2/ALPHA-KINASE, CASEIN KINASE, 2 SER/THR KINASE
1325	1aq1		196	503	0			129.37	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMR score	SEQFOL D score	Compound	PDB annotation
1325	1bi8	A	197	493	8e-86			122.26	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE, CYCLIN-INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN-DEPENDENT KINASE, CYCLIN-DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1325	1bix	A	192	499	1.3e-94			133.76	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1325	1cmk	E	160	503	3.2e-49			102.41	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) ICMK 4 TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37)(CAPK) ICTP 3 (CATALYTIC SUBUNIT) 1ICTP 4	
1325	1ctp	E	165	503	3.2e-49			102.34	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1325	1hcl		196	503	0			141.19		SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1325	1ian		180	567	0			118.03	P38 MAP KINASE; CHAIN: NULL;	TRANSFERASE JNK3;
1325	1jnk		180	563	4.8e-100			136.46	C-JUN N-TERMINAL KINASE;	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	PMF score	SEQFFOL D score	Compound	PDB annotation
								CHAIN: NULL;	
1325	1kob	A	170	522	9.6e-53		106.60	TWITCHIN; CHAIN: A, B;	TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1325	1p38	*	179	570	0		151.09	MAP KINASE P38; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1325	1pme		190	568	0		128.85	ERK2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1325	1tki	A	194	519	1.1e-44		99.53	TITIN; CHAIN: A, B;	TRANSFERASE, SERINE KINASE, TITIN, MUSCLE, AUTONHIBITION
1325	3erk		181	509	0		140.42	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1327	1cs8	A	1	350	0		368.72	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
1328	1cs8	A	19	391	0		412.39	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
1333	1edh	A	65	269	8e-50		124.30	E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1333	1nej	A	64	268	8e-52			129.50	N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1335	1adl	3	133	9.6e-56				158.94	LIPID-BINDING PROTEIN ADIPOCYTE LIPID-BINDING PROTEIN COMPLEXED WITH ARACHIDONIC 1ADL 3 ACID 1ADL 4	
1335	1hmr	3	133	6.4e-58				146.24	LIPID-BINDING PROTEIN FATTY ACID BINDING PROTEIN (HUMAN MUSCLE, M-FABP) COMPLEXED 1HMR 3 WITH ONE MOLECULE OF ELAIDIC ACID 1HMR 4	
1335	1pmp	A	3	133	3.2e-55			161.49	CELLULAR LIPOSOLIC TRANSPORT PROTEIN P2 MYELIN PROTEIN (P2) 1PMP 3	
1340	1a12	A	11	409	1.6e-78			141.30	REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A, B, C,	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCL1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER
1345	1a45	1	148	1.4e-61				122.87	GAMMAF CRYSTALLIN; CHAIN: NULL	EYE LENS PROTEIN EYE LENS PROTEIN
1345	1a5d	A	1	148	4.9e-63			121.88	GAMMAE CRYSTALLIN; CHAIN: A, B	EYE LENS PROTEIN EYE LENS PROTEIN
1345	1am m	1	148	3.2e-65				125.68	GAMMA B-CRYSTALLIN; CHAIN: NULL;	CRYSTALLIN GAMMA II- CRYSTALLIN EYE LENS PROTEIN, CRYSTALLIN
1345	1bd7	A	1	147	1.6e-39			80.96	CIRCULARLY PERMUTED BB2-CRYSTALLIN; CHAIN: A, B;	EYE-LENS PROTEIN EYE-LENS PROTEIN, BETA-CRYSTALLIN B,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1345	1elp	A	1	148	1.3e-62		122.84	GAMMA-D CRYSTALLIN; CHAIN: A, B	EYE-LENS PROTEIN, 2 MULTIGENE FAMILY
1345	1got	B	48	388	9.6e-31		60.77	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	EYE LENS PROTEIN EYE LENS COMPLEX (GTP-BINDING/TRANSDUCER) BETA 1; TRANSDUCIN BETA SUBUNIT; GAMMA 1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROOTRIMER 2 SIGNAL TRANSDUCTION
1345	2bb2	1	148		1.6e-47		99.58	EYE LENS PROTEIN BETA-B2-CRYSTALLIN 2BB2_3	
1352	2fha	6	177	8e-73			273.99	FERRITIN; CHAIN: NULL;	IRON STORAGE IRON STORAGE
1353	1qub	A	184	484	1.6e-11		84.05	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTIDOMAIN, MEMBRANE ADHESION
1363	1awc	B	38	192	1.6e-39		64.05	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1363	1bd8	2		161	8e-30		54.79	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1363	1bix	B	1	165	8e-29			55.34	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEINKINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEINKINASE)
1363	1bu9	A	31	212	1.6e-34			54.53	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C, CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1363	1ih6	A	5	162	8e-34			54.88	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A; B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1363	1lkn	D	73	307	4.8e-38			67.03	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1363	1myo		39	156	3.2e-25			53.66	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1363	1nfi	E	31	243	1.6e-38			64.27	NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B; D; I-KAPPA-B-ALPHA; CHAIN: E; F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1366	1dqv	A	143	415	8.5e-91	0.64	1.00		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1366	1dqv	A	144	415	3.2e-46	0.49	1.00		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PWIF score	SEQFOL D score	Compound	PDB annotation
1366	1rsy		134	270	3.4e-40	0.40	1.00		CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN) (CALB) 1RSY 3	
1366	1rsy		134	270	3.4e-40			122.64	CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN) (CALB) 1RSY 3	
1368	1bu7	A	42	505	1.6e-92			197.06	CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN. P450 REMARK
1368	1oxa		23	504	3.2e-31			67.59	CYTOCHROME P450 ERYF; 1OXA 5 CHAIN: NULL 1OXA 6	OXIDOREDUCTASE (OXYGENASE)
1372	1bg2		2	340	8e-89			210.20	KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN. ATPASE, MICROTUBULE ASSOCIATED
1372	1bg2		4	340	8e-89	0.54	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN. ATPASE, MICROTUBULE ASSOCIATED
1372	1cz7	A	1	340	6.8e-79	0.65	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1372	1cz7	A	1	341	3.2e-72	0.46	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1372	1cz7	A	1	342	6.8e-79			156.19	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1372	2kin	A	2	252	1.2e-28			139.58	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN CYTOSKELETON
1372	2kin	A	4	252	3.2e-57	0.25	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN CYTOSKELETON
1372	2kin	A	6	252	1.2e-58	0.29	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN CYTOSKELETON
1372	2kin	B	265	352	3.4e-28	-0.01	0.98		KINESIN; CHAIN: A, B;	MOTOR PROTEIN CYTOSKELETON
1372	2kin	B	265	358	8e-27	-0.02	0.99		KINESIN; CHAIN: A, B;	MOTOR PROTEIN CYTOSKELETON
1372	2ncd	A	1	339	1.6e-72	0.46	1.00	KINESIN MOTOR NCD; CHAIN: A;	KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
1372	2ncd	A	1	340	1.6e-72			152.53	KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
1372	3kar	5	338	5.1e-74				185.05	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1372	3kar	6	339	6.4e-72	0.31		1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN KAR3, KINESIN RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
1372	3kar	B	7	338	5.1e-74	0.50	1.00	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	KINESIN-LIKE PROTEIN KAR3; CONTRACTILE PROTEIN, KAR3, CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN	
1372	3kin	B	269	352	1.4e-26	0.19	0.99	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	
1372	3kin	B	269	384	3.2e-26	-0.10	0.98	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	
1373	1a4y	A	123	448	4.8e-12	0.19	0.04	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	
1373	1a4y	A	134	545	4.8e-09	0.26	-0.05	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	
1373	1a4y	A	45	361	9.6e-14	0.10	0.00	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	
1373	1a4y	A	63	230	1e-19	0.29	0.37	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
1373	1a9n	A	114	264	5.1e-19	0.66	0.42		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	A	65	220	3.4e-22	0.43	0.17		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	A	90	231	3.4e-19	0.55	0.65		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	C	114	264	3.4e-18	0.48	0.53		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	C	65	220	1.4e-22	0.24	0.04		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	C	90	231	3.4e-19	0.66	0.55		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	16ih	A	294	387	6.8e-14	0.33	0.77		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1373	16ih	A	295	427	1.7e-10	0.37	0.25		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1373	1bpv		421	506	3.4e-07	-0.04	0.07		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN, TITIN, FIBRONECTIN TYPE III

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1373	1cs6	A	286	388	8.5e-15	0.01	-0.05	AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1373	1cs6	A	295	409	3.4e-12	0.31	0.19	AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1373	1cvs	C	306	389	8.5e-14	0.65	1.00	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1373	1cvs	D	296	383	1.2e-14	0.29	0.57	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1373	1d0b	A	152	310	6.4e-26	0.02	0.05	INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	176	332	8e-24	0.09	-0.15	INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	37	211	1.4e-22	0.13	0.57	INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	423	547	1.6e-14	0.05	-0.19	INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	79	265	8e-22	0.31	0.30	INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1dce	A	32	95	9.6e-09	-0.43	0.23	RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOIL D score	Compound	PDB annotation
1373	1dce	A							CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	2.0 A 2 RESOLUTION, N- FORMYL METHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1373	1ds9	A	37	171	8e-08	-0.03	0.15		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYL METHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1373	1ev2	E	292	383	5.1e-14	0.13	-0.08		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1373	1ev2	G	296	387	6.8e-16	0.22	0.13		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1373	1fqv	A	64	231	1.7e-13	0.26	0.54		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1373	1fs2	A	53	231	3.4e-18	0.03	0.31		SKP2; CHAIN: A, C, SKP1;	LIGASE CYCLIN A/CDK2-
										LIGASE CYCLIN A/CDK2-

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
								CHAIN: B; D;	ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCP, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1373	1hnf			303	405	1.7e-08	0.39	0.27	T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (HUMAN) IHNF 3
1373	Inct			292	383	6.8e-19	0.56	0.31	TITIN; CHAIN: NULL; MUSCLE PROTEIN CONNECTIN, NEUTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1373	1tnm			305	383	1.7e-16	0.60	0.76	MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58
1373	1tff			424	502	3.4e-07	-0.29	0.40	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1ITF 3
1373	1vca	A		297	394	1.7e-11	0.46	0.16	HUMAN VASCULAR CELL ADHESION MOLECULE-1; 1VCA 4 CHAIN: A; 1VCA 5 1VCA 15
1373	1wio	A		280	411	3.4e-12	0.37	0.00	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;
1373	1yrg	A		132	362	1.1e-09	0.04	-0.14	GTPASE-ACTIVATING PROTEIN RNA1 SCHPO; TRANSCRIPTION RNA1; RANGA; GTPASE-ACTIVATING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOOL D score	Compound	PDB annotation
									CHAIN: A; B;	FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2-RICH REPEAT PROTEIN, TWINNING, 3-HEMIEDRAL TWINNING, 3-MEROHEDRAL TWINNING, MEROHEDRAL
1373	2bnh	•	45	359	1.4e-18	0.04	0.03		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1373	2bnh		47	231	1.7e-23	0.13	0.06		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1373	2dli	A	294	396	3.4e-11	0.20	-0.05		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1373	3ncm	A	296	383	3.4e-17	0.92	0.35		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1374	1cun	A	65	293	0.0017			61.31	ALPHA SPECTRIN; CHAIN: A, B; C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
1374	1cz7	A	1	131	5.1e-34	-0.46	0.66		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1374	Iquu	A	53	295	3.4e-05			66.44	HUMAN SKELETAL MUSCLE ALPHA-ACTinin 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-Helix COILED COIL, CONTRACTILE PROTEIN
1374	1s1g			36	318	0.0017		65.31	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1374	2kin	A	1	42	5.1e-15	-0.55	0.12		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	2kin	B	55	141	1.7e-27	-0.41	0.81		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	2kin	B	55	154	1.7e-27			65.43	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	3kar		1	127	1e-30	-0.52	0.60		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1374	3kin	B	59	142	6.8e-25	-0.15	0.86		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	3kin	B	59	176	6.8e-25			68.48	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1376	1cej	A	323	405	5.1e-19	-0.02	0.03		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGFR-LIKE DOMAIN, EXTRACELLULAR, MODULAR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMIF score	SEQTOL D score	Compound	PDB annotation
										PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1cej	A	364	435	6.8e-17	-0.11	0.41	MEROZOITE SURFACE PROTEIN 1; CHAIN: A;		SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1cej	A	403	481	5.1e-09	0.08	-0.14	MEROZOITE SURFACE PROTEIN 1; CHAIN: A;		SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1cej	A	45	128	5.1e-21	0.09	0.53	MEROZOITE SURFACE PROTEIN 1; CHAIN: A;		SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1d4v	A	631	733	1.4e-08	0.30	-0.13			APOTOSIS TRAIL; DR5; LIGAND-INDUCING LIGAND; CHAIN: B; DEATH RECEPTOR 5; CHAIN: A;
1376	1dqh	A	181	252	5.1e-14	0.76	0.78	THROMBOMODULIN; CHAIN: A;		JELLY-ROLL, TNF-R 2 SUPERFAMILY, APOPTOSIS
1376	1dqh	A	321	406	5.1e-18	0.30	0.15	THROMBOMODULIN; CHAIN: A;		MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTIKOAGULANT, GLYCOSYLATION
										MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
										ANTICOAGULANT, GLYCOSYLATION
1376	1dq b	A	400	485	5.1e-10	-0.07	0.00		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
1376	1dq b	A	44	131	5.1e-18	0.25	0.21		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
1376	1edm	B	403	433	3.4e-07	-0.14	0.23		FACTOR IX; CHAIN: B; C;	COAGULATION FACTOR CRYSTAL STRUCTURE, EPIDERMAL GROWTH FACTOR, EGF, 2 CALCIUM- BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX, COAGULATION FACTOR
1376	1f7e	A	403	433	5.1e-07	0.09	0.04		BLOOD COAGULATION FACTOR VII; CHAIN: A;	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE DOMAIN, BLOOD 2 CLOTTING
1376	1fjs	L	216	254	1.2e-12	0.66	0.23		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1fjs	L	284	335	3.4e-20	0.27	0.42		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1fjs	L	327	374	1.7e-17	-0.13	0.25		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1fjs	L	407	445	1.4e-15	0.08	0.94		COAGULATION FACTOR XA; CHAIN: A; COAGULATION	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1376	1fjs	L	49	90	1.7e-12	0.83	0.59		FACTOR XA; CHAIN: L;	COAGULATION COFACTOR, PROTEASE
1376	1hcg	B	217	254	3.4e-12	0.50	0.46		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1hcg	B	286	334	1.2e-18	0.34	0.33		COAGULATION FACTOR XA IHCG 3	BLOOD COAGULATION
1376	1hcg	B	407	445	8.5e-15	0.45	0.89		COAGULATION FACTOR XA IHCG 3	BLOOD COAGULATION
1376	1hcg	B	49	90	5.1e-12	0.45	0.95		COAGULATION FACTOR XA IHCG 3	BLOOD COAGULATION
1376	1kg	L	327	374	3.4e-18	0.01	0.31		FACTOR XA; CHAIN: H, L; ANTIKOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, PROTEASE PROTEASE/INHIBITOR
1376	1kg	L	407	445	6.8e-15	-0.06	0.82		FACTOR XA; CHAIN: H, L; ANTIKOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1376	1kg	L	49	90	5.1e-12	0.66	0.34		FACTOR XA; CHAIN: H, L; ANTIKOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1376	1klo		135	322	6.8e-14	0.47	-0.11		LAMMIN; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1376	1klo		286	433	1.7e-20	0.16	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1376	1klo		626	787	8.5e-10	0.38	0.00		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1376	1px	L	121	234	1.7e-14	0.04	0.01		FACTOR IXA; CHAIN: C,L.; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1376	1px	L	289	427	3.4e-27	0.02	0.23		FACTOR IXA; CHAIN: C,L.; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1376	1px	L	41	152	8.5e-26	0.21	0.89		FACTOR IXA; CHAIN: C,L.; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1376	1qfk	L	131	226	1.4e-22	0.28	0.37		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: I; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPETIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	177	252	8.5e-16	0.18	0.72		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
								COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; C;	PROTEASE
1376	1qfk	L	286	389	3.4e-26	-0.11	0.22	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	326	419	1.5e-21	-0.01	0.29	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	367	445	1e-18	0.22	0.99	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	48	141	1.7e-24	0.12	0.92	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	89	189	6.8e-23	-0.29	0.52	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1376	1qub	A	41	444	1.7e-46	0.02	-0.18	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTIDOMAIN, MEMBRANE ADHESION
1376	1rfn	B	175	228	1e-13	0.24	0.35	COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	1rfn	B	285	339	3.4e-19	0.29	-0.01	COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	1rfn	B	407	445	3.4e-11	0.13	0.94	COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	1rfn	B	49	102	8.5e-12	0.67	-0.15	COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	1sfp		805	918	3.4e-21	0.64	0.48	ASFP; CHAIN: NULL;	SPERMADHESIN ACIDIC SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID PROTEIN, ASFP, CUB DOMAIN, X-RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR
1376	1spp	B	809	922	3.4e-22	0.37	0.65	MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-I; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-II; CHAIN: B	COMPLEX (SEMINAL PLASMA PROTEIN/SPP) SEMINAL PLASMA PROTEINS, SPERMADHESINS, CUB DOMAIN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEIN/SPP)

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1376	1tpg		68	158	1.5e-21	0.05	0.04		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
1376	1xka	L	131	230	1.7e-15	0.09	0.59		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	182	254	1.7e-15	-0.01	0.43		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	286	380	5.1e-20	0.25	0.69		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	367	444	3.4e-19	0.28	0.40		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	48	145	3.4e-22	0.01	0.55		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1381	1a06		205	530	5.1e-62	-0.04	0.71		CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1381	1a06		236	534	5.1e-62			109.19	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE;	KINASE KINASE, SIGNAL TRANSDUCTION,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	PsiBlast Verify score	PMF score	SEQOFOL D score	Compound	PDB annotation
1381	1a60			194	550	6.8e-40		CHAIN: NULL; PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	CALCIUM/CALMODULIN TRANSFERASE/PROTEIN SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1381	1bi8	A		204	485	5.1e-41	0.21	1.00	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D; COMPLEX (KINASE/INHIBITOR)
1381	1bix	A		198	495	1.2e-46		92.79	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, P19INK4D; CHAIN: B; COMPLEX (INHIBITOR PROTEINKINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEINKINASE)
1381	1bkx	A		199	485	1.2e-46	0.40	1.00	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, P19INK4D; CHAIN: B; COMPLEX (INHIBITOR PROTEINKINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEINKINASE)
1381	1csn			203	469	6.8e-48	0.06	0.74	CASEIN KINASE-1;1CSN 4 TRANSFERASE(PHOSPHOTRANSFERASE) CAMP.
1381	1ctp	E		169	524	3.4e-71		154.37	DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4 TRANSFERASE(PHOSPHOTRANSFERASE) CAMP.
1381	1ctp	E	•	196	498	3.4e-71	0.41	1.00	DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1381	1hcl		202	495	1.7e-53	0.39		(CATALYTIC SUBUNIT) I CTP 4 HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1381	1hcl		202	499	1.7e-53			115.78 HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1381	1ian		183	555	3.4e-40			92.87 P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1381	1ian		203	475	3.4e-40	0.01	0.88	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1381	1jnk		185	577	1.7e-46			112.39 C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1381	1jnk		203	512	1.7e-46	0.21	1.00	C-JDN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1381	1kob	A	170	570	1.7e-68			127.80 TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1381	1kob	A	205	493	1.7e-68	0.52	1.00	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOLD score	Compound	PDB annotation
1381	3erk		198	498	8.5e-53	0.54	1.00		EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	INTRASTERIC REGULATION TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1381	3erk		213	562	8.5e-53			98.67	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1384	1a07	E	52	210	9.6e-54	0.39	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1384	1a07	E	52	210	9.6e-54			128.38	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1384	1bd2	E	52	210	3.2e-66	0.48	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1384	1bd2	E	52	210	3.2e-66			143.49	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	PMIF score	SEQFOL D score	Compound	PDB annotation
1384	1bec	•	52	210	6.4e-66			CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	RECEPTOR T CELL RECEPTOR IBEC
1384	1bec		53	210	6.4e-66	0.49	1.00	14.3; D T CELL ANTIGEN RECEPTOR; IBEC 5 CHAIN: NULL; IBEC 6	RECEPTOR T CELL RECEPTOR IBEC 14
1384	1fyt	E	53	210	8e-60	0.25	1.00	14.3; D T CELL ANTIGEN RECEPTOR; IBEC 5 CHAIN: NULL; IBEC 6	RECEPTOR T CELL RECEPTOR IBEC 14
1384	1ter	B	50	210	9.6e-64	0.43	1.00	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN; DR CHAIN: A; HLA CLASS II HISTOCOMPATIBILITY ANTIGEN; DR-1 CHAIN: B; HEMAGGLUTININ HA1 PEPTIDE CHAIN; CHAIN: C; T-CELL RECEPTOR ALPHA CHAIN; CHAIN: D; T-CELL RECEPTOR BETA CHAIN; CHAIN: E;	IMMUNE SYSTEM HLA-DRI, DRA; HLA-DR1, DRB1 0101; TCR HA1.7 ALPHA CHAIN; TCR HA1.7 BETA CHAIN; PROTEIN-PROTEIN COMPLEX; IMMUNOGLOBULIN FOLD
1384	1ter	B	51	210	9.6e-64		131.76	ALPHA, BETA T-CELL RECEPTOR CHAIN: A; B;	RECEPTOR TCR, T-CELL, GLYCOPROTEIN, SIGNAL
1388	1a4y	A	21	309	3.2e-17	0.04	-0.11	RIBONUCLEASE INHIBITOR; CHAIN: A; ANGIOGENIN; CHAIN: B; E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE); COMPLEX (RI-ANG) HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1388	1a9n	A	26	156	3.4e-21	0.43	-0.01	U2 RNA HAIRPIN IV; CHAIN: Q,	COMPLEX (NUCLEAR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMTF score	SEQFOIL D score	Compound	PDB annotation
1388 1a9n	A	46	155	4.8e-06	0.28	0.19		R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388 1a9n	A	4	121	1.5e-20	0.48	0.65		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388 1a9n	C	24	106	1.3e-05	0.51	0.51		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388 1a9n	C	26	156	1.2e-21	0.41	-0.08		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388 1a9n	C	46	155	4.8e-06	0.42	0.06		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388 1a9n	C	4	121	6.8e-20	0.67	0.89		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388 1cs6	A	77	280	0.00034	-0.15	0.07		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1388 1d0b	A	19	194	6.4e-27	0.50	0.77		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1388 1d0b	A	4	128	1.4e-12	0.27	0.89		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF score	SEQPOL D score	Compound	PDB annotation
1388	1d0b	A	63	216	1.4e-25	0.28	0.43		INTERNALIN B; CHAIN: A;	ADHESION
1388	1d0b	A	87	236	3.2e-25	-0.05	0.04		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1388	1dce	A	21	127	3.2e-11	0.27	0.90		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYL METHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1388	1dce	A	46	170	1.6e-12	0.59	0.96		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYL METHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1388	1ds9	A	103	236	6.4e-13	0.08	-0.02		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1388	1f01	A	41	103	3.2e-06	-0.05	0.40		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1388	1f01	A	89	171	4.8e-07	-0.06	0.10		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1388	1f01	B	41	103	3.2e-06	0.26	0.04		NUCLEAR RNA EXPORT	RNA BINDING PROTEIN TAP (NFX1);

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOLE score	Compound	PDB annotation
1388	1fpv	A	1	173	1.4e-09	0.29	-0.08		FACTOR 1; CHAIN: A, B;	RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1388	1fqv	A	20	213	1.6e-14	0.12	0.10		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1388	1fqv	A	22	298	4.8e-11	0.08	-0.15		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1388	1fs2	A	11	128	3.4e-12	0.21	0.09		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1388	1fs2	A	20	213	1.6e-14	0.04	0.03		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1388	2bmh		5	131	1.7e-19	0.07	-0.12		RIBONUCLEASE INHIBITOR;	ACETYLATION RNASE INHIBITOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
								CHAIN: NULL;	RIBONUCLEASE/ANGIOTENSIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1388 2bh		74	439	3.2e-20	0.06	-0.15		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR; RIBONUCLEASE/ANGIOTENSIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1389 1klo		476	643	1.6e-13	0.05	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1392 1aj4		10	114	3.2e-23	-0.36	0.01		TROPONIN C; CHAIN: NULL;	muscle protein CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1392 1atk8		2	61	3.2e-22	0.21	0.48		CALMODULIN; CHAIN: NULL;	CALMODULIN C-TERMINIC- DOMAIN, RESIDUES 1 - 75; CERIUM-LOADED, CALCIUM-BINDING PROTEIN
1392 1cdm	A	2	117	4.8e-33	-0.32	0.16			
1392 1cll		1	132	3.2e-38				CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4 CALMODULIN (VERTEBRATE) ICLJ 3	
1392 1cll		2	117	3.2e-38	-0.37	0.11		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
1392 1dtl	A	10	117	1.6e-21	-0.54	0.12		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX- TURN-HELIX
1392 1exr	A	2	117	1.6e-35	-0.22	0.23		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation	
1392	1tcf	1		139	3.2e-28		56.30	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION	
1392	1tcf	2		111	3.2e-28	-0.35	0.11	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION	
1392	1tnx	2		111	8e-24	-0.32	0.33	TROPONIN C; CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14	
1392	1top	1		141	4.8e-28		51.47	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3		
1392	1top	2		111	4.8e-28	-0.03	0.36	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3		
1392	1vrk	A		135	1.4e-37		51.68	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN PEPTIDE)	
1392	1vrk	A	2	117	1.4e-37	-0.42	0.27	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN PEPTIDE)	
1396	1b0x	A		934	1000	1.7e-24	1.07	1.00	EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMIF D score	SEQFOL D score	Compound	PDB annotation
1396	1b4f	A	934	999	8.5e-27	0.92	1.00		EPHB2; CHAIN: A, B, C, D, E, F, G, H;	DIMERIZATION DOMAIN, TRANSFERASE
1396	1bj8								GP130; CHAIN: NULL;	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER
1396	1bp3	B	328	531	1.5e-25	-0.06	0.01		GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1396	1bpv		438	536	4.5e-18	0.20	0.60		TITIN; CHAIN: NULL;	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR, HORMONE/GROWTH FACTOR
1396	1byg	A	627	899	3e-93			169.44	C-TERMINAL SRC KINASE; CHAIN: A;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE II
1396	1byg	A	628	897	1.4e-90	0.83	1.00		C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2
1396	1byg	A	629	898	3e-93	0.64	1.00		C-TERMINAL SRC KINASE; CHAIN: A;	STAUROSPORINE, TRANSFERASE
1396	1c8p	A	437	531	6e-19	0.46	1.00		CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2
1396	1cd9	B	328	524	4.5e-35	0.40	0.07		GRANULOCYTE COLONY-STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR;	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN
										CYTOKINE G-CSF; G-CSF-R; CLASS1 CYTOKINE, HEMATOPOIETIC RECEPTOR, SIGNAL

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation	
1396	1cto		454	531	6e-19	0.32	0.63	CHAIN: B; D; GRANULOCYTE COLONY- STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	TRANSDUCTION BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR	
1396	1em	A	338	531	4.5e-22	-0.12	0.28	ERYTHROPOIETIN RECEPTOR; CHAIN: A, B;	CYTOKINE EBP; ERYTHROPOIETIN RECEPTOR, SIGNAL TRANSDUCTION, CYTOKINE 2 RECEPTOR CLASS 1	
1396	1fgf	C	408	531	4.5e-13	-0.05	0.15	PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4- HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE- RECEPTOR COMPLEX	
1396	1fgk	A	617	900	0			179.56	FGF RECEPTOR 1; CHAIN: A, B; PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE,	
1396	1fgk	A	621	895	0	0.91	1.00	FGF RECEPTOR 1; CHAIN: A, B; PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE,	TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE	
1396	1fgk	B	614	899	0			182.22	FGF RECEPTOR 1; CHAIN: A, B; PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE,	TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION,

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1396	1fgk	B	620	895	0	0.87	1.00		FGF RECEPTOR 1; CHAIN: A, B;	RECEPTOR, PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1396	1fmnk								TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, F60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1396	1fna		454	524	1.2e-13	0.39	0.63		CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE II-10 IFNA 3	
1396	1fmf		322	531	3e-26	0.08	-0.05		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1396	1fpu	A	623	897	0	0.71	1.00		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	TRANSFERASE PI50, C-ABL; KINASE, KINASE INHIBITOR, STI-571, ACTIVATION LOOP
1396	1ir3	A	623	910	0		188.00		INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE, TYROSINE KINASE, SIGNAL TRANDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE))
1396	1ir3	A	626	910	0	0.81	1.00		INSULIN RECEPTOR; CHAIN: A;	COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOLD score	Compound	PDB annotation
									PEPTIDE SUBSTRATE; CHAIN: B;	(TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1396	1mfn			331	533	1.3e-25	0.08	0.53	FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1396	Inuk	A	31	202	1.5e-83	0.58	1.00		TYROSINE-PROTEIN KINASE RECEPTOR EPH; CHAIN: A;	TRANSFERASE NUK; TRANSFERASE, EPH RECEPTOR TYROSINE KINASE,
1396	Inuk	A	31	202	1.5e-83			182.17	TYROSINE-PROTEIN KINASE RECEPTOR EPH; CHAIN: A;	TRANSFERASE NUK; TRANSFERASE, EPH RECEPTOR TYROSINE KINASE,
1396	1qcf	A	610	902	0	0.90	1.00		HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1396	1qg3	A	329	534	1.5e-36	0.19	0.22		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1396	1qg3	A	331	522	6.8e-11	0.03	0.18		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1396	1qpc	A	621	900	0	0.97	1.00		LCK KINASE; CHAIN: A;	TRANSFERASE ALPHA BETA FOLD
1396	1qr4	A	331	529	1.5e-30	0.27	-0.03		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1396	1sgg								EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
									TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION, EPH RECEPTORS, TYROSINE 2, PHOSPHORYLATION, SIGNAL TRANSDUCTION, TYROSINE-PROTEIN 3 KINASE
1396	1tff								
1396	1vr2	A	622	897	5.1e-98	0.88	1.00	EPHRIN TYPE-B RECEPTOR 2; CHAIN: NULL;	TYROSINE 2, PHOSPHORYLATION, SIGNAL TRANSDUCTION, TYROSINE-PROTEIN 3 KINASE
1396	2fib	A	326	423	3e-09	0.07	-0.14		
1396	2fib	A	439	529	9e-19	0.36	0.17	FIBRONECTIN; CHAIN: A;	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3
1396	2hft								VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR CHAIN; A, FIBRONECTIN; CHAIN: A;
1396	1akh	A	81	121	6e-05	1.11	0.99		PROTEIN BINDING ED-B, FIBRONECTIN, TYPEII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1401	1au7	A	83	125	0.00015	0.82	0.94	PIT-1; CHAIN: A; DNA; CHAIN: C, D;	PROTEIN BINDING GHF-1; COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										(DNA-BINDING PROTEIN/DNA), PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR
1401	1b72	B	83	125	0.0006	0.27	0.43			HOMEBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA, COMPLEX, DNA-BINDING PROTEIN/DNA CHAIN: E; PROTEIN, PROTEIN/DNA.
1401	1bw5		83	125	6e-05	0.73	0.93			INSULIN GENE ENHANCER PROTEIN ISL-1; CHAIN: NULL; DNA-BINDING PROTEIN, HOMEODOMAIN, LIM DOMAIN
1401	1du6	A	83	127	0.0003	-0.11	0.03			HOMEBOX PROTEIN PBX1; CHAIN: A; HOMEODOMAIN
1401	1fj1	B	83	125	0.0003	0.82	0.99			PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1401	1hdp		83	125	0.00015	0.50	0.80			DNA-BINDING PROTEIN OCT-2 POU HOMEODOMAIN (NMR, AVERAGE STRUCTURE) IHDP 3
1401	1mn_m	C	82	125	0.00015	0.63	1.00			MCM1 TRANSCRIPTIONAL REGULATOR; CHAIN: A, B; MAT ALPHA-2 TRANSCRIPTIONAL REPRESSOR; CHAIN: C, D; STE6 OPERATOR DNA; CHAIN: E, F; COMPLEX (TRANSCRIPTION/HOMEobox/DNA)
1401	1oep		83	125	9e-06	0.28	0.84	OCT-3; 1OCP 5 CHAIN; NULL; 1OCP 6		DNA-BINDING PROTEIN
1401	1pos		83	125	0.0001	0.41	0.96	DNA BOUNDING PROTEIN OCT-1 POU HOMEODOMAIN DNA-BINDING PROTEIN MUTANT		

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
									WITH 1POG 3 ARG GLY SER HIS MET INSERTED AT THE N- TERMINUS AND ASP ILE 1POG 4 INSERTED AT THE C- TERMINUS (NSRGSHMR6)INS(66-D1)1POG 5 (NMR, 13 STRUCTURES)1POG 6	
1403	1a36	A	644	772	5.1e-08	0.03	-0.09		TOPoisomerase I; CHAIN: A; DNA; CHAIN: B, C;	COMPLEX (ISOMERASE/DNA) COMPLEX (ISOMERASE/DNA), DNA, TOPOISOMERASE I
1403	1dn1	B	389	556	0.00017	-0.16	0.00		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1403	1or3	A	527	634	0.00017	-0.13	0.19		APOLIPOPROTEIN E; CHAIN: A;	LIPID BINDING PROTEIN APOE3; LIPID TRANSPORT, HEPARIN-BINDING, PLASMA PROTEIN, HDL, VLDL
1403	1qru	A	367	551	6e-15	-0.12	0.04		HUMAN SKELETAL MUSCLE ALPHA-ACTinin 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-Helix COILED COIL, CONTRACTILE PROTEIN
1404	1c28	A	826	947	1e-27	1.14	0.39		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
1404	1c28	B	827	947	6e-22	0.71	-0.13		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
1404	1c28	C	826	947	4.5e-18	0.84	0.43		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
1404	1cun	A	375	591	6e-12	-0.03	0.29		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1404	1cun	A	436	651	4.5e-07	0.02	0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1404	1fio	A	292	467	6e-07	-0.08	0.19		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1404	1hae		120	150	0.0045	0.07	0.11		HEREGULIN-ALPHA; CHAIN: NULL;	GROWTH FACTOR NEU DIFFERENTIATION FACTOR (RAT), ACETYLCHOLINE GROWTH FACTOR
1404	1hre		120	150	0.0045	0.13	0.25		GROWTH FACTOR HEREGULIN-ALPHA (EPIDERMAL GROWTH FACTOR-LIKE DOMAIN) 1HRE 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1HRE 4	
1407	1b6c	B	25	129	1.4e-09	-0.26	0.12		FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12, SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1407	1fgk	A	22	126	1.7e-05	-0.02	0.04		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
1407	1fmk	22	127	3e-05	0.17	0.36			TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1407	1fpu	A	22	130	1.5e-05	-0.09	0.18		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, ST-571, ACTIVATION LOOP
1407	1pme	21	131	7.5e-06	-0.12	0.37			ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1407	1qcf	A	22	129	9e-05	-0.56	0.11		HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1407	1qpc	A	22	61	7.5e-05	-0.75	0.23		LCK KINASE; CHAIN: A;	TRANSFERASE ALPHA BETA FOLD
1407	3erk	21	126	1.5e-05	-0.35	0.09			EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1408	1a44	2	168	4.5e-70	0.60	1.00			PHOSPHATIDYLETHANOLAMI NE-BINDING PROTEIN; CHAIN: NULL;	LIPID-BINDING PROTEIN PEBP, PBP LIPID-BINDING
1408	1a44	2	168	4.5e-70			267.15		PHOSPHATIDYLETHANOLAMI NE-BINDING PROTEIN; CHAIN: NULL;	LIPID-BINDING PROTEIN PEBP, PBP LIPID-BINDING
1408	1beh	A	3	168	3e-63	0.89	1.00		PHOSPHATIDYLETHANOLAMI NE BINDING PROTEIN; CHAIN: A, B;	LIPID-BINDING LIPID-BINDING, SIGNALLING
1408	1beh	A	3	168	3e-63		271.38		PHOSPHATIDYLETHANOLAMI NE BINDING PROTEIN; CHAIN:	LIPID-BINDING LIPID-BINDING, SIGNALLING

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1410	1a88	A	47	319	0.00015	0.25	0.90		CHLOROPEROXIDASE L; CHAIN: A, B, C;	HALOPEROXIDASE L, BROMOPEROXIDASE L, HALOPEROXIDASE L; HALOPEROXIDASE, OXIDOREDUCTASE
1410	1a8s									HALOPEROXIDASE F; HALOPEROXIDASE; OXIDOREDUCTASE, PROPIONATE COMPLEX
1410	1azw	A	11	319	4.5e-05			60.20	PROLINE IMINOPEPTIDASE; CHAIN: A, B;	AMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS
1410	1azw	A	47	319	4.5e-05	0.00	0.42		PROLINE IMINOPEPTIDASE; CHAIN: A, B;	AMINOPEPTIDASE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS
1410	1b6g		12	325	1.5e-08			61.14	HALOALKANE DEHALOGENASE; CHAIN: NULL;	HYDROLASE HYDROLASE, HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE
1410	1b6g		35	318	1.5e-08	0.13	0.77		HALOALKANE DEHALOGENASE; CHAIN: NULL;	HYDROLASE HYDROLASE, HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE
1410	1cqw	A	10	319	6e-09	0.38	0.99		HALOALKANE DEHALOGENASE; 1- CHLOROHEXANE CHAIN; A;	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE I-S BOND
1410	1cv2	A	47	154	3e-05	-0.16	0.19		HALOALKANE DEHALOGENASE; CHAIN: A;	HYDROLASE LINB, 1,3,4,6- TETRACHLORO-1,4- CYCLOHEXADIENE

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										DEHALOGENASE, LINDANE, BIODEGRADATION, ALPHA/BETA-HYDROLASE
1410	1ek1	A	47	321	1.1e-07	0.12	0.98		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1410	1ek1	B	47	321	3e-07	0.14	0.95		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1410	1hg1	A	47	165	0.003	-0.15	0.41		LIPASE, GASTRIC; CHAIN: A, B;	HYDROLASE LIPASE
1410	1qge	D	47	195	0.0006	-0.13	0.10		TRIACYL GLYCEROL HYDROLASE; CHAIN: D;	HYDROLASE PSEUDOMONADACEAE, CIS-PEPTIDE, CLOSED CONFORMATION, 2 HYDROLASE, LID
1410	1qj4	A	47	316	9e-09	0.02	0.37		HYDROXYNITRILE LYASE; CHAIN: A;	LYASE OXYNITRILE LYASE; OXYNIRILASE, CYANOGENESIS, CYANHYDRIN FORMATION, LYASE
1410	1qr1	A	11	321	1.2e-05			57.92	PROLYL AMINOPEPTIDASE; CHAIN: A;	HYDROLASE ALPHA BETA, HYDROLASE FOLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 SERRATIA, MINOPEPTIDASE
1410	1qr1	A	74	319	1.2e-05	-0.51	0.12		PROLYL AMINOPEPTIDASE; CHAIN: A;	HYDROLASE ALPHA BETA, HYDROLASE FOLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 SERRATIA, MINOPEPTIDASE
1410	4lip	D	47	155	9e-05	0.06	0.05		TRIACYL GLYCEROL HYDROLASE; CHAIN: D, E;	HYDROLASE, LIPOSOME, PSEUDOMONADACEAE, COVALENT INTERMEDIATE, 2 TRIGLYCERIDE ANALOGUE, ENANTIOSELECTIVITY
1415	1dn1	B	384	513	0.00045	-0.02	0.09		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A;	ENDOCYTOSIS/EXOCYTOSIS NSSEC1; PROTEIN-PROTEIN

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1418	1alh	A	401	426	0.00015	0.11	0.01		CHAIN: B;	COMPLEX, MULTI-SUBUNIT
1418	1alh	A	404	485	3e-24	0.05	0.95		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1418	1mey	C	403	486	4.5e-25				QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1418	1mey	C	404	485	4.5e-25	-0.09	1.00	76.20	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA, INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	1mey	C	432	543	6e-23	-0.01	0.53		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA, INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	1mey	C	461	575	1.2e-21	-0.31	0.06		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA, INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	1sp1		522	547	1.2e-06	-0.44	0.25		SPIR3; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1418	1ubd	C	408	543	1.4e-24	-0.01	0.07		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
								ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YTNG-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION (REGULATION/DNA))
1418	1ubd	C	432	575	1e-24	-0.42	0.03	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YTNG-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION (REGULATION/DNA))
1418	2adr		461	549	4.5e-14	0.04	0.17	ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1418	2adr		522	575	1.4e-12	-0.41	0.03	ADRI1; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1418	2dtp	A	522	577	1.2e-14	-0.69	0.06	COMPLEX(TRANSCRIPTION REGULATION(DNA)) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
1418	2gji	A	369	485	3e-20	-0.05	0.47	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1418	2gji	A	404	575	4.5e-33	-0.16	0.25	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF D score	SEQFOL D score	Compound	PDB annotation
1419	laut	L	118	259	3e-15	0.04	0.17		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	BINDING PROTEIN/DNA)
1419	1dan	L	136	270	1.5e-15				BLOOD COAGULATION COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN II A; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)	
1419	1dx5	I	136	232	1e-17	0.14	0.24		BLOOD COAGULATION FACTOR VIIA, CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C; (DFRCMK) WITH CHAIN: C;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTIKOAGULANT COMPLEX, 2 ANTIFBRINOLYTIC COMPLEX
1419	1dx5	I	168	264	1.1e-13	0.33	0.55		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTIKOAGULANT COMPLEX, 2 ANTIFBRINOLYTIC COMPLEX
1419	1ext	A	31	191	3e-16	0.14	-0.11		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOOL D score	Compound	PDB annotation
1419	1ext	A	61	243	3e-16		59.06	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	PROTEIN SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1419	1klo		125	298	9e-22	0.05	-0.01	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1419	1klo		29	185	4.5e-26	0.54	-0.01	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1419	1klo		61	247	4.5e-27	0.51	0.23	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1419	1klo	L	77	234	4.5e-27	0.07	-0.09	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1419	1pxk	L	13	128	1.1e-25			FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/E/GF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1419	1pxk	L	205	298	6e-21	-0.04	0.18	FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/E/GF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1419	1pxk	L	38	165	6e-30		67.49	FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/E/GF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1419	1pxk	L	76	223	6e-30	-0.30	0.31	FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
									CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN	
1419	1pp2	R	39	169	1.5e-19	0.24	-0.18		HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A=2=(E.C.3.1.1.4) IPP2_4	
1419	1qfk	L	109	216	3e-15	0.11	0.30		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1419	1qfk	L	145	247	7.5e-15	0.09	-0.06		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1419	1skz		141	271	3e-15	-0.17	0.98		ANTISTASIN; CHAIN: NULL;	
1419	1skz		66	179	3e-15			55.31	ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR; FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1419	1tpg		156	237	4.5e-20	0.31	0.53		T-PLASMINOGEN ACTIVATOR	PLASMINOGEN ACTIVATION

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
									F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	
1419	1tpg		220	297	4.5e-15	-0.31	0.18		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
1419	1tpg		29	109	7.5e-19	0.14	-0.01		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
1419	1vep	A	145	273	9e-16	0.02	-0.19		PHOSPHOLIPASE A2; CHAIN: A, B;	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE
1419	1vap	A	81	236	7.5e-16	0.04	-0.19		PHOSPHOLIPASE A2; CHAIN: A, B;	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE
1419	1ypi		81	204	3e-19	0.07	-0.18		PHOSPHOLIPASE A2 INHIBITOR; CHAIN: NULL	NEUROTOXIN PHOSPHOLIPASE A2 INHIBITOR, X-RAY STRUCTURE, RECOGNITION, 2 MOLECULAR EVOLUTION, NEUROTOXIN
1419	1xka	L	145	222	9e-14	0.17	0.37		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1419	9wga	A	13	142	1.5e-24	0.23	0.30		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1421	1amo	A	272	539	6.8e-40	-0.16	0.01		NADPH-CYTOCHROME P450 REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE CPR, P450R; X- RAY CRYSTALLOGRAPHY, FLAVOPROTEIN, NITRIC OXIDE SYNTHASE, 2 OXIDOREDUCTASE
1421	1fb3	A	252	538	5.1e-57	-0.13	0.21		CHLOROPLAST FERREDOXIN- NADP+ OXIDOREDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE TWO DOMAIN MOTIF, ROSSMANN FOLD

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1421	1fnb		252	538	3.4e-55	0.09	0.01	OXIDOREDUCTASE (NADP+(A)FERREDOXIN(NADP+ FERREDOXIN(NADP+ OXIDOREDUCTASE (FERREDOXIN REDUCTASE, IFNB 3 FLAVOENZYME) (E.C.1.18.1.2) IFNB 4 IFNB 72	
1421	1qfj	A	246	510	3.4e-31	-0.07	0.07	FLAVIN REDUCTASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE RIBOFLAVIN, FLAVIN REDUCTASE, FERREDOXIN REDUCTASE 2 SUPERFAMILY, OXIDOREDUCTASE
1421	1qfz	A	252	537	1.7e-54	-0.14	0.43	FERREDOXIN:NADP+ REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE FNR; FLAVOENZYME, PHOTOSYNTHESIS, ELECTRON TRANSFER, HYDROGEN 2 TRANSFER, OXIDOREDUCTASE
1421	1que		258	538	3.4e-49	0.06	-0.03	FERREDOXIN--NADP+ REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE FNR; OXIDOREDUCTASE, FLAVOPROTEIN, NADP, FAD, THYLAKOID MEMBRANE, 2 HYCOBILISOME, FNR, NADP+ REDUCTASE
1421	2cnd		244	502	3.4e-57	0.00	-0.12	OXIDOREDUCTASE (NITROGENOUS ACCEPTOR)	
								NADH-DEPENDENT NITRATE REDUCTASE (CYTOCHROME B REDUCTASE 2CND 3 FRAGMENT)(E.C.1.6.6.1) COMPLEXED WITH FAD 2CND 4 (SYNCHROTRON X-RAY DIFFRACTION) 2CND 5	
1426	1alh	A	265	347	1.5e-45			QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),

SFQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
								OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1426	1mey	C	236	318	1e-51		103.77	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	
1426	1tf6	A	236	402	1.7e-38		99.56	TFIIL; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX TRANSCRIPTION REGULATION(DNA), RNA POLYMERASE II, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1426	1ubd	C	211	318	6e-54		88.81	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX TRANSCRIPTION REGULATION(DNA)
1426	2gli	A	207	347	6e-69		93.51	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1434	1bg1	A	191	320	0.00034	0.41	0.27	STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	COMPLEX (TRANSCRIPTION FACTOR/DNA) TRANSCRIPTION FACTOR, PROTEIN-DNA COMPLEX, CYTOKINE 2 ACTIVATION, COMPLEX (TRANSCRIPTION FACTOR/DNA)
1434	1bz4	A	187	304	1.7e-05	0.25	0.13	APOLIPOPROTEIN E, CHAIN; A;	LIPID BINDING PROTEIN APO-E3;

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
									LIPID TRANSPORT, LIPID TRANSPORT, HEPARIN-BINDING, PLASMA 2 PROTEIN, HDL, VLDL REMARK
1434	1cii		1	514	1.5e-27			115.08	COLICINIA; CHAIN: NULL; TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
1434	1cun	A	127	372	7.5e-11	0.07	-0.01	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1cun	A	228	430	3e-10	0.28	0.00	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1cun	A	253	475	3e-11	0.10	0.10	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1cun	A	389	494	6e-06	0.40	0.40	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1dn1	B	296	481	6e-11	0.05	0.18	SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1434	1ez3	A	316	449	1.5e-08	0.18	-0.18	SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1434	1ez3	A	364	486	1.5e-08	0.36	-0.02		SYNTAXIN-1A; CHAIN: A, B, C;	BUNDLE ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1434	1qsa	A	2	514	3e-20			104.88	SOLUBLE LYtic TRANSGLYCOSYLASE SLT70; CHAIN: A;	TRANSFERASE ALPHA- SUPERHELIX, TRANSFERASE
1434	1quu	A	228	464	1.5e-18	0.21	0.27		HUMAN SKELETAL MUSCLE ALPHA-ACTinin 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL CONTRACTILE PROTEIN
1434	1quu	A	332	481	1.2e-09	0.25	-0.17		HUMAN SKELETAL MUSCLE ALPHA-ACTinin 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN
1434	1sig		225	512	3e-09			89.88	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE REGULATION
1434	1sig		293	514	3e-09	0.14	0.21		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE REGULATION
1437	1rgp		1126	1315	1.5e-53			105.03	RHO GAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE- ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1437	1tx4	A	1129	1329	4.5e-58			106.55	P50-RHO GAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATOR(Proto-oncogene)) GTPase-activating protein RHOGAP; COMPLEX (GTPASE ACTIVATION PROTO-ONCOGENE), GTPase, 2 TRANSITION STATE, GAP
1441	1ann		7	299	0			431.20	ANNEXTIN IV; LANN 5 CHAIN:	CALCIUM/PHOSPHOLIPID-BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1452	1cvj	H	77	159	1.7e-19	0.81	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(* AP* A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1; PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	1d8z	A	73	153	1.7e-21	0.73	1.00		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1452	1hal	1	151	1.7e-35	0.06	0.07			HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1452	1hal		75	157	1.7e-21	0.87	1.00		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1452	2u2f	A	74	158	3.4e-19			50.59	SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPlicing, U2 SNRNP, RBD, RNA-BINDING PROTEIN
1452	2up1	A	1	155	1.2e-36	0.28	0.64		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1452	3sxl	A	1	144	3.4e-32	0.13	0.04		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPlicing INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3

SEQ NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMIF D score	SEQFOL D score	Compound	PDB annotation
1452	3sxl	A	76	230	1.4e-20	0.20	0.69		SEX-LETHAL; CHAIN: A, B, C;	DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1452	3sxl	A	7	146	3.4e-32		53.30	SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPlicing INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	
1454	1c0t	A	345	668	3.4e-85	-0.04	0.87	HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON-NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN	
1454	1c0t	B	346	668	5.1e-88	-0.17	0.84	HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON-NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN	
1454	1c1c	B	345	668	0	-0.09	0.99	HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON-NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN	
1454	1c9r	A	341	671	1.7e-91	-0.06	0.99	HIV-1 REVERSE TRANSCRIPTASE (CHAIN A); SYSTEM/DNA HIV-1 RT; HIV-1 RT;	TRANSFERASE/IMMUNE	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast Verify score	PMF score	SEQ FOL D score	Compound	PDB annotation
								CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H; DNA (5'; CHAIN: T; DNA (5'; CHAIN: P;	HIV, REVERSE TRANSCRIPTASE, MET184I/L,E, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M184L TRANSFERASE/IMMUNE 3 SYSTEM/DNA
1454	1c9r	B	341	668	8.5e-98	-0.13	0.99	HIV-1 REVERSE TRANSCRIPTASE (CHAIN A); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H; DNA (5'; CHAIN: T; DNA (5'; CHAIN: P;	HIV, REVERSE TRANSCRIPTASE, MET184I/L,E, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M184L TRANSFERASE/IMMUNE 3 SYSTEM/DNA
1454	1har	*	341	551	3.4e-65	0.05	1.00	REVERSE TRANSCRIPTASE HIV-1 REVERSE TRANSCRIPTASE (AMINO-TERMINAL HALF) (FINGERS IHAR 3 AND PALM SUBDOMAINS) (RT21.6) (E.C.2.7.7.49) IHAR 4	REVERSE TRANSCRIPTASE
1454	1mmi		326	570	1e-59	0.36	1.00	MMLV REVERSE TRANSCRIPTASE; 1MML 4 CHAIN: NULL; 1MML 5	REVERSE TRANSCRIPTASE
1454	1mmi		326	571	1e-59		199.34	MMLV REVERSE TRANSCRIPTASE; 1MML 4 CHAIN: NULL; 1MML 5	REVERSE TRANSCRIPTASE
1454	1rh	A	341	668	0	0.00	1.00	HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4 CHAIN: A, B; 1RTH 5	NUCLEOTIDYL TRANSFERASE HIV-1 RT; 1RTH 6 HIV-1 REVERSE TRANSCRIPTASE 1RTH 15
1454	1rh	B	345	668	0	-0.17	1.00	HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4	NUCLEOTIDYL TRANSFERASE HIV-1 RT; 1RTH 6 HIV-1 REVERSE

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	Verify store	PMF score	SEQFOLE score	Compound	PDB annotation
1454	1vrt	A	345	668	0	-0.04	1.00		CHAIN: A; 1RTH 5	TRANSCRIPTASE 1RTH 15
1454	1vrt	B	345	668	0	-0.09	1.00		HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1454	3hvvt	B	342	668	3.4e-100	-0.11	0.66		HIV-1 REVERSE TRANSCRIPTASE; 1VRT 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1454	3hvvt	B	342	672	3.4e-100				NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE (E.C.2.7.7.49) 3HVT 3	
1455	1dus	A	6	135	5.1e-13	-0.00	-0.08		NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE (E.C.2.7.7.49) 3HVT 3	
1456	1igl		25	94	6.8e-25	0.37	1.00		MJ0882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII
1456	1igl		25	94	6.8e-25					
1456	1igl		25	94	6.8e-25					
1456	3lri	A	16	93	4.5e-25	-0.15	1.00		GROWTH FACTOR INSULIN-LIKE GROWTH FACTOR II (IGF-II, IGF-2) 1IGL 3 (NMR, 20 STRUCTURES) 1IGL 4 1IGL 78	
1458	2occ	E	46	132	6.8e-37	0.33	1.00		CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J,	OXIDOREDUCTASE FERROCYTOCHROME C:OXYGEN

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast score	PMF score	SEQFOL D score	Compound	PDB annotation
								K, L, M, N, O, P, Q,	OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C2 OXIDASE
1458	2occ	E	46	132	6.8e-37		115.24	CYTOCHROME COXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q,	OXIDOREDUCTASE; FERROCYTOCHROME C:OXYGEN OXIDOREDUCTASE; CYTOCHROME(C)-OXYGEN, CYTOCHROME C2 OXIDASE
1459	1avs	A	601	640	0.009	0.64	1.00	TROPONIN C; CHAIN: A, B;	muscle contraction muscle contraction, calcium- activated, tropinin, e-f hand 2 calcium-binding protein
1459	1awj		-						
1459	332		408	3e-11	0.01	0.29	ITK; CHAIN: NULL;	TRANSFERASE IL-2 INDUCIBLE T- CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE	
1459	1b8q	A	248	365	1e-18	-0.14	0.87	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
1459	1be9	A	248	341	3.4e-16	0.28	0.92	PSD-95; CHAIN: A; CRIP7; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
1459	1g2b	A	334	392	3e-12	-0.25	0.54	SPECTRIN ALPHA CHAIN; CHAIN: A;	METAL BINDING PROTEIN CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, SH3 2 DOMAIN, CYTOSKELETON
1459	1gbr	A	340	408	4.5e-11	-0.16	0.13	SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQTOL D score	Compound	PDB annotation
1459	1gfc								WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	
1459	1gky								ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	
1459	1gky		479	663	1e-10	0.36	0.66			
1459	1gky		480	662	1e-68	0.80	1.00	146.00	TRANSFERASE GUANYLATE KINASE (E.C.2.7.4.8) COMPLEX WITH 1GKY 3 GUANOSINE MONOPHOSPHATE 1GKY 4	
1459	1i16		253	345	1.1e-16	0.31	0.95		TRANSFERASE GUANYLATE KINASE (E.C.2.7.4.8) COMPLEX WITH 1GKY 3 GUANOSINE MONOPHOSPHATE 1GKY 4	
1459	1kwa	A	254	337	3e-17	0.19	1.00		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
1459	1kwa	A	257	338	3.4e-16	0.07	0.98		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
1459	1pdr		253	342	3.4e-14	0.19	0.96		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
									SIGNAL TRANSDUCTION HDLG, DHR 3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsiBlast	Verify score	PIPER score	SEQOFOL D score	Compound	PDB annotation
1459	1pwt		347	408	4.5e-11	0.46	0.58		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
1459	1qau	A	254	362	1.5e-17	0.13	0.98		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	OXIDOREDUCTASE BETA-FINGER
1459	1qav	A	250	336	4.5e-16	0.24	1.00		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERO-DIMER
1459	1qkw	A	350	408	3e-11	0.10	0.48		ALPHA II SPECTRIN; CHAIN: A; CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN	
1459	1qly	A	349	408	1.3e-10	0.41	0.47		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
1459	1sem	A	350	408	1.5e-10	-0.10	0.41		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 1G-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
1459	1tud		334	392	6e-13	0.22	0.40		ALPHA-SPECTRIN; CHAIN: NULL;	CYTOSKELETON CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, 2 SH3 DOMAIN, CYTOSKELETON
1459	1ukz		477	659	1.4e-07	0.10	0.69		TRANSFERASE URIDYLATE KINASE (E.C.2.74.4.) COMPLEXED WITH ADP AND AMP 1UKZ 3.	
1459	1zak	A	482	662	1.2e-05	0.02	0.22		ADENYLYLATE KINASE; CHAIN:	TRANSFERASE ATP-AMP.

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMF score	SEQFFOL D score	Compound	PDB annotation
1459	3adk							A, B;	PHOSPHOTRANSFERASE, TRANSFERASE
1459	3pdz	A	253	332	1.5e-13	0.32	1.00	TRANSFERASE PHOSPHOTRANSFERASE ADENYLATE KINASE (E.C.2.7.4.3) 3ADK ⁴	
1459	3tmk	C	479	662	9e-10	0.28	0.04	TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A; HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS, SPECIFICITY 2 OF BINDING	
1459	4tmk	A	478	662	7.5e-16	-0.03	0.19	THYMIDYLATE KINASE, CHAIN: A, B, C, D, E, F, G, H; PHOSPHOTRANSFERASE, TRANSFERASE ATP-DTMP PHOSPHOTRANSFERASE	KINASE KINASE, PHOSPHOTRANSFERASE, CHAIN: A;
1461	1bg3	A	1	493	0	1.13	1.00	HEXOKINASE; CHAIN: A, B; HEXOKINASE, PHOSPHOTRANSFERASE; HEXOKINASE.	HEXOKINASE ATP:D-HEXOSE-6-PHOSPHOTRANSFERASE; HEXOKINASE.
1461	1bg3	A	1	499	0			459.01	HEXOKINASE; CHAIN: A, B; HEXOKINASE, PHOSPHOTRANSFERASE; HEXOKINASE, PHOSPHOTRANSFERASE
1461	1cza	N	1	501	0	1.07	1.00	N;	HEXOKINASE TYPE I; CHAIN: N; TRANSFERASE STRUCTURALLY HOMOLOGOUS DOMAINS
1464	1a0j	A	30	239	1.4e-80	0.88	1.00	TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
1464	1a0j	A	30	239	1.4e-80		104.84	TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
1464	1a0l	A	30	233	1.7e-74	0.50	1.00	BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TRYPSIN, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1464	1a0l	A	30	239	1.7e-74		97.00	BETA-TRYPTASE; CHAIN: A, B,	SERINE PROTEINASE TRYPSIN-LIKE

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast Verify score	PMIF score	SEQFOL D score	Compound	PDB annotation
1464	1bru	P		239	1.7e-75	0.64	1.00	C, D;	SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA, SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
1464	1bru	P		239	1.7e-75		115.93	ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
1464	1dpo			239	1.7e-79		98.94	TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, PANCREAS, ZYMOGEN, 2 SIGNAL, MULTIGENE FAMILY
1464	1fuj	A *		237	6e-71		200.42	PR3; CHAIN: A, B, C, D;	HYDROLASE (SERINE PROTEASE) MYELOBLASTIN; HYDROLASE, SERINE PROTEASE, GLYCOPROTEIN, ZYMOGEN, SIGNAL
1464	1mct	A		239	8.5e-83	0.74	1.00	COMPLEX(PROTEINASE/INHIBITOR) TRYPsin (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER 1MCT 3 GOURD IMCT 4	
1464	1mct	A		239	8.5e-83		103.86	COMPLEX(PROTEINASE/INHIBITOR) TRYPSin (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER 1MCT 3 GOURD IMCT 4	
1464	1ppf	E		237	1e-65		315.52	HYDROLASE(SERINE PROTEINASE) HUMAN LEUKOCYTE ELASTASE (HLE) (NEUTROPHIL ELASTASE (NHE)) 1PPF 3 (E.C.3.4.21.37) COMPLEX WITH THE THIRD DOMAIN OF TURKEY 1PPF 4 OVOMUCOID INHIBITOR (OMTKY3) 1PPF 5	